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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 ∕ Compugen
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Human 15 kDa selen Mouse 15 kDa selen Human secreted pro Human 5' EST relat Human prostate can Drosophila melanog Gene 1 human secreted pro Arabidopsis thalia Arabidopsis thalia
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Peptide
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chali	AAG41381	21	691	8.3	69
ָח	AAG70749	22	682	8 . 3	69
opsis	AAG41382	21	668	8.3	69
1	AAB21149	21	538	8.3	69
Œ.	AAG41383	21	515	•	69
sequ	AAB67880	22	1288	8.4	69.5
	AAR49039	15	961	8.4	69.5
	AAR34934	14	656	8.4	9
poly	AAM40358	22	1112	8.4	70
Human SUMO-1 SEQ I	AAG78297	22	1112	•	70
Drosophila melanog	ABB58666	22	656	•	70.5
Human autoantigen	AAG80205	22	979	•	71
_	AAY06606	20	979		71
Human polypeptide	AAM4 0531	22	896	•	71
Novel protein kina	AAB65606	22	890	8.5	71
æ	AAM38745	22	890	•	71
	AAG30333	21	421	•	71
€O.	AAG30334	21	351	•	71
Drosophila melanog	ABB61103	22	1175	•	
C glutamicum prote	AAG92241	22	679	8.6	
Neisseria gonorrhe	AAY74485	21	243		73.5
en fr	AAR09418	11	677	•	
Sequence of 70kd p	AAP80088	9	676	9.1	75.5
P	AAR03925	Ľ	669	9.1	
	AAG42015	21	401	9.1	
Arabidopsis thalia	AAG42016		316	•	75.5
B. subtilis dihydr	AAU01251		558	9.2	76.5
Drosophila melanog	ABB70557		523	•	77
uzi HSP.	AAR03926		657		79.5
5' EST	AAY65389		50	17.8	148
н	AAB44006		34	20.5	170
	AAG43256		159	٠	•
	Ç		158	27.3	226.5
Arabidopsis thalia	AAG08632	21	158	27.3	226.5

Minimum DB Maximum DB

seq seq

Scoring table:

Searched:

Title: Perfect score:

OM protein -

Database

ALIGNMENTS

Selenoprotein; selenium; differential expression; tumour; human; prostate cancer; diagnosis; polymorphism. Human 15 kDa selenoprotein (USSH) US DEPT HEALTH & HUMAN SERVICES AAY32112 standard; (first entry) 98US-0080850 99WO-US07560 93 /note= "signal peptide" 27..162 Location/Qualifiers 1..26 /label= OTHER /note= "selenocysteine" Protein; 162 ₽ ä

Result No.

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226.5 226.5 226.5

99.8 57.0 57.0 57.0 37.4 36.3 36.3 27.3 27.3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer. Claimed methods of detecting the presence, or of quantifying the level of expression, of the 15 kDa selenoprotein involve contacting a sample with a specific binding agent, such as a polyclonal antibody or monoclonal antibody. that specifically binds to the 15 kDa selenoprotein. A claimed method for dietary regulation comprises detecting an abnormally low expression of a 15 kDa selenoprotein in a subject and, if the level is below normal, enhancing the level by providing additional selenium in the diet. The susceptibility to cancer of a subject having an increased predetermined genetic susceptibility to cancer is reduced by administering the 15 kDa selenoprotein or by overexpressing the selenoprotein using gene therapy.
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15 ki
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14-OCT-1999
                                                                                                                                                                 Selenoprotein;
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                           W09951637-A1
                                                                                                                                                  prostate
                                                                                                                                                                                          Mouse 15
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                                                                                 Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  differentially expressed in cancer cells, such as cancer cells includes a selenocysteine residue at position 93 that is encoded a TGA codon in the cDNA (see AAZ34464). Polymorphisms in the
                                                                                                                       musculus
                                                                                                                                                                                                                                                                                                    N
                                                                                                                                                                                                                                                                                                                                                         VRGSDPVLKLLDDNGNIAEELSILKWNTDSVEEFLSEKLERI 162
                                                                                                                                                                                                                                                                                                                                                                                                 lqldpdcrgccqeeaqfetkklyagailevcgxklgrfpqvqafvrsdkpklfrglqiky
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                                                                                                                                                  cancer;
                                                                                                                                                                                         kDa selenoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence represents a human 15 kDa selenoprotein that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55; 67pp;
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                                                                                                                                                              selenium; differential expression;
                                                                               Location/Qualifiers 93
                                                                                                                                                  diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.8%; Score 829; DB 21; 100.0%; Pred. No. 8.8e-88;
                                                    "selenocysteine
                                                                     OTHER
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o or treating or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 162;
                                                                                                                                                              tumour;
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Matches
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                                                                                                                                                                                                                                                                                          is differentially expressed in cancer certs, such as concerded in children at position 93 that is encoded by a TGA codon in the cDNA (see AAZ34468). Polymorphisms in the human 15 kDa selenoprotein gene are associated with susceptibility to cancer. Claimed methods of detecting the presence, or of quantifying the level of expression, of the 15 kDa selenoprotein involve contacting a sample with a specific binding agent, such as involve contacting a sample with a specific binding agent, such as
                                                                                                                                                   a polyclonal antibody or monoclonal antibody, that specifically binds to the 15 kDa selenoprotein. A claimed method for dietary regulation comprises detecting an abnormally low expression of a mammalian 15 kDa selenoprotein in a subject and, if the level is below normal, enhancing the level by providing additional selenit in the diet. The susceptibility to cancer of a subject having an increased predetermined genetic susceptibility to cancer is reduced by administering a mammalian 15 kDa selenoprotein or by
                                                                                              Sequence
                                                                                                                                     overexpressing the selenoprotein using gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 60; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated selenoprotein polypeptides, used to develop products for detecting susceptibility to or treating cancers e.g. prostate cancers {\tt detecting}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                             present sequence represents a mouse 15 kDa selenoprotein that
lifferentially expressed in cancer cells, such as cancer cells
      150;
                      Similarity
                                                                                                  162 AA;
    Conservative
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                      90.7%;
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                  Score 754; DB 21;
Pred. No. 4.3e-79;
    Mismatches
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KW Huma
KW diag
KW deve
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KW inmu
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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemi developmental abnormality; foetal deficiency; blod; allergy; renal; Immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;

leukaemia;

Human secreted

protein encoded by gene 70 clone HMSGT42.

25-MAR-1999 AAW67876

(first entry)

cognitive disorder; schizophrenia; prostate; obesity; osteoporosis; arthritis; testis; lung; thyroiditis; tl

thyroid;

osteoclast; thymu hyroid; digestion;

thymus

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                                                                                                                          This sequence represents a secreted human protein encoded by the gene clane detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAX00602) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 87 novel genes and their fragments (nucleic acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polymetides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 87 polynucleotides, based on which tissues they are most highly expressed in (see AAX00611 for described uses).
                                                                                                                                                                                                                                                                                                                                                                                                           Rosen
                                                                                                                                                                                                                                                                                                                           New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                       Brewer LA,
Greene JM,
                                                                                                                                                                                                                                                                                                    Claim 11; Page 310; 385pp; English.
                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-070066/06.
N-PSDB; AAX00680.
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21-MAR-1997;
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                                                                                                      Sequence
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21-MAR-1997;
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Similarity
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-0048131.
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5.2e-47;
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Query Match Best Local S Matches 91

Similarity

57.0%; 98.9%;

91;

Conservative

0

Score 474; DB Pred. No. 5.4e 0; Mismatches

DB 21; ۲.

Length Indels

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CC AAZ42255 to AAZ43075 represent novel 5' expressed sequence tag (EST)
CC sequences, corresponding to human secreted proteins. AAY64651 to
CC AAZ43052. The 5' ESTs can be used for producing secreted human gene
CC products. They can be used to identify and isolate 5' untranslated
CC regions (UTRs) and upstream regulatory regions which control the
CC location, development stage, rate, and quantity of protein synthesis, as
CC well as stability of mRNA. The ESTs are also useful as probes for
CC chromosome mapping, and to obtain full length cDNA clones. The ESTs can
CC diagnostic procedures to identify individuals, or in
CC diagnostic procedures to identify individuals having genetic diseases
CC gene therapy protocols. The nucleic acids encoding signal peptides can be
CC used for directing extracellular secretion of a polypeptide or the
CC insertion of a polypeptide into a membrane, or importing a polypeptide
CC treating a variety of human conditions. Secreted proteins have
CC therapeutic value, and the identification of reas secretion have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
AAY65395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel secreted protein 5' expressed sequence tag sequences used in diagnostic, forensic, gene therapy, and chromosome mapping procedures
Sequence
                                                                                               therapeutic value, and the identification of new secreted proteins is valuable. AAZ42249 to AAZ42264 and AAX646444 to AAX64650 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 818; 837pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEST ) GENSET
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28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-OCT-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |ene therapy;
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95
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chromosome mapping; upstream regulatory sequence;
atlon; development; protein synthesis; stability;
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98US-0069047
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                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome polynucleotides may be used for detection of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; prostate cancer; prostate cancer antigen; detection; neuroprotective; cytostatic; cardioactive; immunomodulatory; vulnerary; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; neural; immune; reproductive; restrointestinal; pulmonary; cardiovascular; proliferative of gastrointestinal; pulmonary; cardiovascular; proliferative of the control of the cardiovascular; proliferative of the cardiovascular of the card
                                                                                                                                                                                                                                                                                                     gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAr16506 to AAr16514 to AAB57303 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                      or research purposes. The prostate cancer antigens may be used disorders such as neural, immune, muscular, reproductive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAR-2001
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                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF15566 to AAF16505 encode the human prostate cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 2183-2184; 2338pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human prostate cancer antigen protein sequence SEQ ID NO:1710.
                                                                                                                                                                                                                                                                                   invention.
                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
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                          1 MAAGPSGCLVPAFGKRLLLATVLQAVSAFGAEFSSEACRELGFSSNLLCSSCDLLGQFNL
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infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF16335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        such as prostate cancer
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                                                                                                                                                                                                                         124 AA;
                                                                                 Conservative
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                                                                                                        57.0%;
98.9%;
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nephrotropic; antiinfective; gynaecological;
                                                                                                        Score 474; DB 21; Pred. No. 7.8e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neural; immune;
cardiovascular;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reproductive; renal; proliferative disorder;
                                                                                                                               Length 124;
                                                                              Indels
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                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophila. The inventuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data specification, but
                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 16749; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid genes from Drosophila and
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11-JUL-2000;
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                     108 DKPKLFRGLQIKYVRGSDPVLKLLDDNGNIAEELSILKWNTDSVEEFLSEKLER 161
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grpakfpnlqikyvrgldpvvklldasgkvqetlsitkwntdtveeffethlak 114
                                                                                                 \verb|mcsscek|| \texttt{ldtikpqckqcctldqqpaaqrtyakailevctckfraypqiqafiqs}|
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DB; ABL07422.
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                                                                                                                                                                                                                                  37.4%;
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                                                                                                                                                                                                       ; Score 311; DB 22;
; Pred. No. 7.1e-28;
17; Mismatches 38;
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RESULT

AAB75288

AAB75288 standard; Protein; 60

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CC include, immunosuppressive; antiarthritic; antirheumatic;
CC antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
CC nootropic; neuroprotective; antibacterial; virucide; fungicide;
CC opthalmalogical; and vulnerary activity. The protein and polynucleotide
CC sequences, their agonists and antagonists may be useful for treating,
CC preventing and diagnosing diseases and disorders such as autoimmune
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders
CC e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. cerebral ischaemia,
CC infections caused by bacteria, viruses and fungi and ocular disorders
CC e.g. corneal infection. The polypeptides can also be used to aid wound
CC e.g. corneal infection. The polypeptides can also be used to aid wound
CC e.g. corneal infection organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities. Included in the invention are
CC oligonucleotides Aar63780 - Aar63788 and peptide AAB75239 which are used
CC in the identification and characterisation of the DNA and protein
  Query Match
Best Local Similarity
Matches 60; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             which encode human secreted proteins AAB75260 - AAB75287. Included in th invention are protein sequences AAB75288 - AAB75341 which are fragments of the secreted proteins and amino acid sequences with which these fragments share homology. Examples of the activities of the proteins and polynic lectides and the activities of their agonists and antagonists
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Score 302; DB
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CC which encode human secreted proteins AAB75280. AAB75287. Included in the CC invention are protein sequences AAB75281. Included in the CC invention are protein sequences AAB75281. AAB75341 which are fragments CC of the secreted proteins and amino acid sequences with which these CC fragments share homology. Examples of the activities of the proteins and CC polynucleotides and the activities of their agonists and antagonists (CC include, immunosuppressive; antiarthritts; antirhemmatic; cardiant; vasotropic; cerebroprotective; (CC antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; (CC opthalmalogical; and vulnerary activity. The protein and polynucleotide sequences, their agonists and antagonists may be useful for treating, (CC preventing and diagnosing diseases and disorders such as autoimmune CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders (C. e.g. neoplasms of the breast or liver, cardiovascular disorders (C. e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, (C. e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, (C. e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, (C. e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, (C. e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, (C. e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, (C. e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, (C. e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, (C. e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, (C. e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, (C. e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, (C. e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, (C. e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, (C. e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, (C. e.g. cardiac arr
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N-PSDB; AAF63789.
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Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid molecules encoding human secreted proteins, used
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Similarity 100.0%;
60; Conservative
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9908-0125748
9908-0125788
9908-0126785
9908-0127462
9908-0128344
9908-0129845
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0; Mismatches
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9908-0138044
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Query Match
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16-AUG-1999;
17-AUG-1999;
18-AUG-1999;
20-AUG-1999;
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11-AUG-1999;
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9908-0160815
9908-0161404
  27.3%;
32.9%;
  Score
Pred.
  226.5; DB 21;
No. 4.6e-18;
               Length 149;
RESULT 10
AAGO8633
ID AAGO8663
XX AAGO866
XX AAGO866
XX AAGO866
XX DT 17-OCT
DE Arabic
XX Prote:
KW hybric
XX termin
OS Arabic
XX Ep103
XX Ep103
XX PD 06-SE
XX 25-FE
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99US-0121825 99US-0123180

990S-0123180 990S-0123548 990S-0126788 990S-0126785 990S-0128724 990S-0128724 990S-0130419 990S-0130419 990S-0130449 990S-0131449 990S-0131449 990S-0132485 990S-0132485 990S-0132485 990S-0132486 990S-0132487 990S-0132487 990S-0134281 990S-0134281 990S-0134281 990S-0134281 990S-0134281 990S-0134281 990S-013421 990S-013421

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
Arabidopsis thaliana
                                                               Arabidopsis
                                                                                      17-OCT-2000
                                                                                                                              AAG08633 standard; Protein; 155
                                                                                                          AAG08633;
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| | | | : : : : | | : : gehkesiridnwkrehllqymrekvk
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                                                             thaliana
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                                                                                   (first
                                                                                   entry)
                                                              protein
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                                                              fragment SEQ
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                                                               A
                                                                NO:
                                                                                                                                                                                                                                                                                                                  54;
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5-AUG-	4-AUG-1999;	4-AUG-1999;	R 02-AUG-1999; 99US-0146389.	2-AUG-1999;	2-AUG-1999;	3-JUL-1999;	7-JUL-1999;	7-JUL-1999:	7-JUL-1999;	5-JIII1999:	3-JUL-1999:	3-JUL-1999;	3-JIII1999;	2-JUL-1999:	2-JUL-1999;	27011999:	2-JUL-1999:	21-JUL-1999;	21-301-1999;	21	0-JUL-1999; 0-JUL-1999;	20-1111-1999	20-,71111999	19-TIII - 1999.	19-701-1999;	19-JUL-1999;	19-JUL-1999;	19-JUL-1999;	16-JUL-1999;	16-JUL-1999;	15-JUL-1999;	1999;	1,666	2-JUL-1999;	9-JUL-1999;	8-JUL-1999;	6-JUL-1999;	2-JUL-1999;	1-JUL-1999;	1-JUL-1999;	0-JUN-1999;	9-JUN-1999;	8-JUN-1999;	4-JUN-1999;	1999;	3-JUN-1999:	7-TUN-1999;	8-JUN-1999;	8-JUN-1999;	8-JUN-1999;	1999,	1999;	•	1999;	1999:	18-JUN-1999;	18-JUN-1999;	17-JUN-1999;	16-JUN-1999;	16-JUN-1999;	14-JUN-1999;	10-JUN-1999:	9	08 - TIN- 1999	7 - TIN-1999;		5
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Query Match	22 001	29-0CT-10		28-OCT-19	26-OCT-19	26-0CT-19	26-00T-10	25-00m-10	25 - OCT - 19	25 OCT 15	22 OCT 10	22-OCT-10	01-E00-10	21-0CT-19	21-0CT-19	21-0CT-19	21-0C1-10 71-100-11	21-0CT-19	18-OCT-19	16 OCT - 19	14-OCT-19	14 -OCT - 19	14 -OCT - 19	14 -OCT - 19	13-0CT-19	13-0CT-19	13-OCT-19	12-OCT-19	08-OCT-19	07-OCT-19	06-OCT-19	05-OCT-19	04-OCT-19	29-SEP-19	28-SEP-19	24-SEP-19	23-SEP-19	22-SEP-19	20-SEP-19	16-SEP-19	15-SEP-19	13-SEP-19	10-SEP-19	07-SEP-19	01-SEP-10	31-AUG-16	27-AUG-19	27-AUG-19	27-AUG-19	26-AUG-10	23-AUG-19	23-AUG-19	20-AUG-19	20-AUG-19	20-AUG-19	17-AUG-19	16-AUG-19	13-AUG-19	13-AUG-19	12-AUG-10	11-AUG-10	10-AUG-15	09-AUG-19	06-AUG-15	06-AUG-19	05-AUG-19	
27.3%; Score 226.5; DB 21; Length 155;	2200 010	9905-016	99US-0161992.	99US-016	99US-016	9905-016	99175-016	9905-016	9905-016	9905-016	9905-016	010-016	00TO - 010	990S-016	9908-016	89/09T0-S066	9905-0160769	910-SU66	9908-0159584	9908-0159638	9908-0159637	305-015	30 S - 01	9908-01	TO-5066	99US-01	9908-01	9908-015	99US-015	99US-015	9905-015	99US-015	. 99US-015	9908-019	99US-015	9905-019	99US-01	99US-015	9908-019	99US-019	9908-01	9908-019	99US-01	9905-01	9905-01	990S-018	99us-01	99US-01	99US-019	10-5056	9075-016	9908-01	99US-01	99US-01	710-5066	9908-01	9908-01	,10-Sn66	99US-01	7.01-S1166	9905-01	99115-01	710-SD66	10-S066	9905-01	99US-01	

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RESULT 13
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netic mapping; gene expression control;
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S-0147204. S-0147302. S-0147192.

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gene expression control;
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Best Local
in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsortatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antiinflammatory; antithyroid; antialtergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; limmune disorder; haematopoietic cell disorder; autoimmune disorder; artiversus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                      Claim 11; Page 2132; 2352pp; English.
                                                                                                                                                                                                                          Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing {
m e.g.} cancer -
                                                                                                                                                                                                                                                                              WPI; 2000-587533/55.
N-PSDB; AAC78215.
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29-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer associated protein sequence SEQ ID NO:1451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48;
                                                                                                                                      to AAC78448 encode the human cancer associated proteins given 398 to AAB44239. The proteins can have activities based on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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99US-0162142.
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                                                                              Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoletic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC7849 to AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                           the present invention.
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Query Match
Best Local Similarity

Sequence

34

8

Matches 34; Conservative 20.5%; 0 Score 170; DB 21; Pred. No. 2.1e-12; Mismatches Length 34; 0; Gaps

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Search completed: September 18, Job time: 3876 sec 2002, 16:32:01

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Minimum DB
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	ALIGNMENTS	AAR13231	AAR11602	AAY33968	ABB62713	AAG84961	AAR13308	AAR13303	AAR79835	ABG09902	AAB76657	AAG91651	AAW44120	AAR13296	AAW38289	AAW53232	AAR13236	ABB59876	ABB67773	AAM51207	AAR31014	AAW23088	AAG07225	AAG07226	ABG07527	AAG43256	AAG43257	AAG08632	AAM42036	AAG43258	AAG08633	AAR13304	AAG08634	94	AAY27650
		CFTR delta I507.	Mutant cystic fibr	CFTR protein seque	Drosophila melanog	Shrimp white spot	3659 del	CFTR Y1092X. Homo	Truncated cystic f	Novel human diagno	Corynebacterium gl	C glutamicum prote	12	CFTR G542X. Homo	Murine N-acetylgal	idi		Drosophila melanog	Drosophila melanog	Rat Csk binding pr								Arabidopsis thalia	m.		hali	CFTR 556 del A. H	Arabidopsis thalia	nibacteri	Human secreted pro

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RRSULT AAY32112 ID AAY32112 ID AAY32112 ID AAY3 212 ID AAY3 XX AAY Ol-re CONTRACT CO
                                                                                             06-APR-1998;
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(USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                              06-APR-1999;
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27..162
/note= "mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                               /label= OTHER
/note= "selenocysteine"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "mature protein (specifically claimed
Claim 12")
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Human 15 kDa selenoprotein

01-FEB-2000 AAY32112;

(first entry)

AAY32112 standard; Protein; 162 AA.

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Matches 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-013045/01.
N-PSDB; AAZ34464.
14-OCT-1999
                             WO9951637-A1
                                                                                                                                                             prostate cancer;
                                                                                                                                                                         Selenoprotein; selenium; differential expression; tumour;
                                                                                                                                                                                                        Mouse 15
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                                                                                    Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     differentially expressed in cancer cells, such as cancer cells. includes a selenocysteine residue at position 93 that is encoded a TGA codon in the cDNA (see AAZ34464). Polymorphisms in the
                                                                                                                                                                                                                                                                                                                       N
                                                                                                                                musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence represents a human 15 kDa selenoprotein that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vrgsdpvlkllddngniaeelsilkwntdsveeflsekleri 162
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                                                                                                                                                                                                      kDa selenoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 55; 67pp; English.
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                                                                                                                                                                                                                                  (first entry)
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                                                                    93
/label=
                                                                                                Location/Qualifiers
                                                        /note= "selenocysteine"
                                                                                                                                                             diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.4%; Score 161; DB 21; 100.0%; Pred. No. 2.9e-150;
                                                                      OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptides, used to develop products for or treating cancers e.g. prostate cancers
                                                                                                                                                          polymorphism
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                                                                                 Matches
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                                                                                                                                                                                                                         Sequence
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                       CRGCCQEEAQFETKKLYAGAILEVCGXKLGRFPQVQAFVRSDKPKLFRGLQIKYVRGSDP 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67pp; English.
                                                                                                        58.6%; Score 95; 100.0%; Pred. No.
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                                                                              Mismatches
                                                                                                        DB 21;
2.4e-85;
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                                                                                                                                  Length 162
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                                                                              Indels
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RESULT
AAW67876
ID AAW6
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AAW67876 standard; Protein;
                                                           Human secreted
                                                                     25-MAR-1999
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                                                                    (first entry)
                                                          protein encoded by gene 70 clone HMSGT42
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127

VLKLLDDNGNIAEELSILKWNTDSVEEFLSEKLERI 162

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crgccqeeaqfetkklyagailevcgxklgrfpqvqafvrsdkpklfrglqikyvrgsdp 126

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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

W09842738-A1

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Best Local S
Matches 77
                                                                                                                                                                    This sequence represents a secreted human protein encoded by the gene clone detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAX00602) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 87 novel genes and their fragments (nucleic acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polynucleotides. Specific uses are described for each of the 87 polynucleotides, based on which tissues they are most highly expressed in (see AAX00611 for described uses).
                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 310; 385pp; English.
                                                                                                                                                                                                                                                                                                                                                                       disorders,
                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                      New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-070066/06.
N-PSDB; AAX00680.
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30-MAY-1997;
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21-MAR-1997;
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21-MAR-1997;
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                                                                                           Local Similarity
les 77; Conserv
                                          RLILATVLQAVSAFGAEFSSEACRELGFSSNLLCSSCDLLGQFNLLQLDPDCRGCCQEEA 75
Ruben
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                                                                                           Conservative
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97US-0048199.
97US-0048131.
97US-0048135.
97US-0048154.
97US-0048186.
97US-0048187.
97US-0048188.
97US-00481818.
97US-0048351.
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97US-0048355
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97US-0048095.
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97US-0048069.
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97US-0041277.
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100.0%; Pr
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                                                                                          ; Score 77; DB
; Pred. No. 7.2
0; Mismatches
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r DW, Moore PA,
Y, Young P;
                                                                                                   DB 20;
7.2e-68;
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Ni J, Olse
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Query Match
Best Local Similarity
Matches 77; Conserv

47.5%; ilarity 100.0%; Conservative

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Score 77; Pred. No. Mismatches

DB 21; 7.4e-68;

Length Indels

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RESULT
AAY65395
                                                                                                                                                                                              sequences, corresponding to human secreted proteins. AAV64651 to AAV65438 represent the EST-related proteins corresponding to AAAV65438 represent the EST-related proteins corresponding to AAAV2265 to AAX46522. The 5' ESTs can be used for producing secreted human gene products. They can be used to identify and isolate 5' untranslated regions (UTRs) and upstream regulatory regions which control the location, development stage, rate, and guantity of protein synthesis, as well as stability of mRNA. The ESTs are also useful as probes for chromosome mapping, and to obtain full length cDNA clones. The ESTs can also be used in forensic procedures to identify individuals, or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal gene expression. The products may also be used in gene therapy protocols. The nucleic acids encoding signal peptides can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell. The proteins encoded by the EST sequences may be useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability; regulation; identification.
                                                           treating a variety of human conditions. Secreted proteins have therapeutic value, and the identification of new secreted proteins valuable. AAA242249 to AAA242264 and AAY64644 to AAY64650 represent sequences used in the exemplification of the present invention.
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N-PSDB; AAZ43009.
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28-APR-1998;
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human 5' EST related polypeptide SEQ ID NO:1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
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   95
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98US-0069047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuroprotective; cytostatic; vulnerary; gastrointestinal; antibacterial; gene therapy;
                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 2183-2184; 2338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorders such as prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gastrointestinal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins, called prostate cancer antigens, given in AAB56363 to A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAF16335.
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76 QFETKKLYAGAILEVCG
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                                                 intestinal; pulmonary;
infectious disease.
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                                                                                                                                                                                              Similarity
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ROSEN C A.
                                                                                                                                                                                                                                                                                                             124
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                                                                                                                                                                Conservative
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                                                                                                                                                                                           47.5%;
100.0%;
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                                                                                                                                                                                           Score 77;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiovascular; proliferative disorder;
                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      the exemplification
                                                                                                                                                                                           DB 21; I
9.3e-68;
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                                                                                                                                                                                                                                                                                                                                                                                      of the present
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RESULT
AAB75288
e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotraxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. Included in the invention are oligonucleotides AAF63780 - AAF63788 and peptide AAB75239 which are used in the identification and characterisation of the DNA and protein sequences of the invention.
                                                                                                                                                                                                                                                                                    of the secreted proteins and amino acid sequences with which these fragments share homology. Examples of the activities of the proteins and polynucleotides and the activities of their agonists and antagonists include, immunosuppressive; antiarthritic; antirhemmatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; and vulnerary activity. The protein and polynucleotide sequences, their agonists and antagonists may be useful for treating, preventing and diagnosing diseases and disorders such as autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to polynucleotide sequences AAF63789 - AAF63836 which encode human secreted proteins AAF5260 - AAF5287. Included in tlinvention are protein sequences AAF5288 - AAF541 which are fragments of the secreted proteins and amino acid sequences with which these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; autoimmune disease; hyperproliferative disorder; cancer; cardiovascular disorder; cerebrovascular disorder; infection; nervous system disorder; ocular disorder; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preventing, treating 
Parkinson's diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
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ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or ameliorating
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      This invention relates to polynucleotide sequences AAF63789 - AAF63836 CC which encode human secreted proteins AAB75280 - AAB75287. Included in the CC invention are protein sequences AAB75288 - AAB75287. Included in the CC invention are protein sequences AAB75288 - AAB75287. Included in the CC invention are protein sequences with which these CC fragments share homology. Examples of the activities of the proteins and CC polynucleotides and the activities of their agonists and antagonists of include, immunosuppressive; antiarthritic; antirheumatic; CC include, immunosuppressive; antiarthritic; antirheumatic; CC include, immunosuppressive; antiarthritic; antirheumatic; CC include, immunosuppressive; antibatterial; virucide; fungicide; CC include, immunosuppressive; antibatterial; virucide; fungicide; CC opthalmalogical; and vulnerary activity. The protein and polynucleotide cc sequences, their agonists and antagonists may be useful for treating, CC opthalmalogical; and vulnerary activity. The protein and polynucleotide cc sequences, their agonists and antagonists may be useful for treating, CC opthalmalogical; and diseases and disorders such as autoimmune cc diseases e.g. rheumatoid arthritis, hyperproliferative disorders cc. e.g. cardiac arrest, cerebrovascular disorders cc. e.g. cardiac arrest, cerebrovascular disorders cc. e.g. cardiac arrest, cerebrovascular disorders cc. angiogenesis, nervous system disorders e.g. cerebral ischaerder. CC infections caused by bacteria, viruses and fungi and ocular disorders cc. corneal infection. The polypeptides can also be used to ald wound the challenge of brimary tissues, to regenerate tissues and in chemotaxis. The culture of brimary tissues, to regenerate tissues and in chemotaxis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 10; 530pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid molecules encoding human secreted proteins, used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2000; 2000WO-US15135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nervous system disorder; ocular disorder; chemotaxis; food additive
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Parkinson's diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or ameliorating a disorder, e.g. Alzheimer's and cancers \mbox{\ensuremath{^{\circ}}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Komatsoulis
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Pred. No.
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2.6e-51;
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Best Local :
        AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidabetic; antiasthmatic; antirheumatic; antiartritic; antiinflammatory; antithyroid; antirheumatic; antiartritic; coagulant; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating of ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists, and antagonists from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antianglogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. Included in the invention are oligonucleotides AAF63780 - AAF63788 and peptide AAB75339 which are used in the identification and characterisation of the DNA and protein
                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                            Novel isolated nucleic acids comprising sequences encoding useful for treating or diagnosing e.g. cancer -
                                                                                                                                                                                                                                                                                              WPI; 2000-587533/55
N-PSDB; AAC78215.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antidiabetic; antiasthmatic; antirheumatic; antiarthritic; a
antiinflammatory; antithyroid; antiallergic; antibacterial;
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Best Local
regions (UTRs) and upstream regulatory regions which control the location, development stage, rate, and quantity of protein synthesis, as well as stability of mRNA. The ESTs are also useful as probes for chromosome mapping, and to obtain full length cDNA clones. The ESTs can also be used in forensic procedures to identify individuals, or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal gene expression. The products may also be used in the protection of the products of the products may also be used the protection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability; regulation; identification.
                                                                                                                   sequences, corresponding to human secreted proteins. AAY6451 to AAX65438 represent the EST-related proteins corresponding to AAX42265 AAX43052. The 5' ESTs can be used for producing secreted human gene products. They can be used to identify and isolate 5' untranslated
                                                                                                                                                                             AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (EST)
                                                                                                                                                                                                          Claim 3;
                                                                                                                                                                                                                                     diagnostic,
                                                                                                                                                                                                                                                                               N-PSDB;
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28-APR-1998;
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                                                                                                                                                                                                          Page 816-817; 837pp; English.
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                                                                                                                                                                                                                                     forensic,
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98US-0069047
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and chromosome
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ABB63319
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Best Local
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                                                            useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL/16176-ABL30511), expressed DNA sequences (ABL/16176-ABL30511), expressed DNA (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypept into a cell. The proteins encoded by the EST sequences may be usefu treating a variety of human conditions. Secreted proteins have therapeutic value, and the identification of new secreted proteins valuable. AAZ42249 to AAZ42264 and AAY64644 to AAY64650 represent
Sequence
                                        The sequence data for this patent did not form specification, but was obtained in electronic 1
                                                                                                                                                                   The invention relates to an isolated nucleic acid detection
                                                                                                                                                                                          Disclosure; SEQ ID NO 16749; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                        Venter JC,
                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster polypeptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002
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                                                                                                                                                                                                                                       genes from Drosophila
                                                                                                                                                                                                                                                     New isolated nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 kyvrgsdpvlkllddngniaeelsilkw 47
                           ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KYVRGSDPVLKLLDDNGNIAEELSILKW 146
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                                                                                                                                                                                                                                                                                                                       Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                       PWD,
                                                                                                                                                                                                                                      detection reagent for detecting for elucidating cell signalling
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Pred. No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21;
6.4e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID NO 16749.
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                                        format directly from
                                                     part of the printed
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Query Match

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RESULT 1
AAU46002
ID AAU4
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                  CC polypeptides. The proteins and their associated DNA sequences are used in Cc the treatment, prevention and diagnosis of medical conditions caused by CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne, CC pustulosis, hypertosis and osteomyelitis), uveitis and endopthalmitis. CC P. acnes is also involved in infections of bone, joints and the central CC nervous system, however it is particularly involved in the inflammatory CC lesions associated with acne vulgaris. A method for detecting the CC presence or absence of P. acnes in a patient comprises contacting a CC sample with a binding agent that binds to the proteins of the invention CC and determining the amount of bound protein in the sample. The CC polypeptides may be used as antigens in the production of antibodies CC specific for P. acnes proteins. These antibodies can be used to CC downregulate expression and activity of P. acnes polypeptides and CC diagnostic agents for determining P. acnes presence, for example, by CC enzyme linked immunosorbent assay (ELISA).

CC Note: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO CC at fig. wipo.int/pub/published_pct_sequences.
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02-JUN-2000;
07-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammatory les dermatological;
                                                                                                                                                                                                                                                                                                                                         Example 1;
                                                                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes polypeptides and nucle vaccinating against and diagnosing infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L'maisonneuve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAPHO syndrome; uveitis; endophi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU46002 standard; Protein; 303
                                                                                                                                                                                                                                                                                                                                                                       treating
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8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; endophthalmitis; bone; joint; central nervous system; ELISA; tory lesion; acne vulgaris; enzyme linked immunosorbent assay; ogical; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                       acne vulgaris
                                                                                                                                                                                                                                                                                                             AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
                                                                                                                                                                                                                                                                                                                                        SEQ ID No 7197; 1069pp; English
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ve J, Zha
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2000US-208841P.
2000US-216747P.
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, Jen S, Carter D;
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RESULT
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Matches 8
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07-NOV-1997;
07-NOV-1997;
07-NOV-1997;
07-NOV-1997;
07-NOV-1997;
17-NOV-1997;
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07-NOV-1997;
07-NOV-1997;
07-NOV-1997;
                                                                                                                                                                                                             New human
disorders
                                                                                                                                                                                                                                                                                                                        Kyaw H, I
Ruben SM,
This sequence represents a secreted human protein encoded by the gene clone detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAX84924) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 125 novel genes and their fragments (nucleic acid sequences: AAX84933-X85057; amino acid sequences AAY27567-Y27933) which are useful for preventing, treating or ameliorating medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; alleray; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
                                                                                                                                                                       Claim 11;
                                                                                                                                                                                                                                                                                                                                                           Carter KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-NOV-1998;
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17-NOV-1997;
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                                                                                                                                                                                                                                                                   1999-337740/28.
DB; AAX85016.
                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN GENOME
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                                                                                                                                                                                                                                                                                                                      Lafleur DW, Moor
, Shi Y, Soppet
                                                                                                                                                                                                         secreted proteins and coding sequences useful for treating of the immune system and hyperproliferative disorders
                                                                                                                                                                       Page 397;
                                                                                                                                                                                                                                                                                                                                                         Ebner R,
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970S-0064983
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97US-0064908.
97US-0064911.
97US-0064912.
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                                                                                                                                                                                                                                                                                                                                          Olsen
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polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosts of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 125 polynucleotides, based on which tissues they are most highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-616774/71.
N-PSDB; AAS59546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAPHO syndrome; synovitis; acne; uveitis; endophthalmitis; bone;
                                                                                                                                                                                                                                                                                                                                                       Sequences AAU39105-AAU68017 represent Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L'maisonneuve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID No 11139; 1069pp; English.
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e J, Zha
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100.0%;
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, Jen S, Carter D;
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Pred. No.
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o. 27;
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25-FEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
25-MAR-1999
25-MAR-1999
26-APR-1999
06-APR-1999
06-APR-1999
16-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
24-APR-1999
25-APR-1999
26-MAY-1999
06-MAY-1999
11-MAY-1999
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11-MAY-1999
11-MAY-1999
11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG08634 standard; Protein; 149 AA.
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                                                                                                                                                                                                                                                                                                                                            25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                 06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
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99US-0130449.
99US-0130510.
99US-0130891.
99US-0132048.
99US-01324407.
99US-0132486.
99US-0132486.
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99US-0132486.
99US-0134219.
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99US-0125788.
99US-0126264.
99US-0126785.
99US-0127462.
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99US-0130077.
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99US-0128714.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein fragment
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100.0%; Pred. No.
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03-JUN 00-JUN 10-JUN 110-JUN 110-JUN 1110-JUN 11110-JUN 1110-JUN	24 - N 25 - N 27 - N 28 - N
04-Jun 1999; 07-Jun 1999; 08-Jun 1999; 08-Jun 1999; 10-Jun 1999; 11-Jun 1999; 11-Ju	24-MAY-1999; 25-MAY-1999; 27-MAY-1999; 28-MAY-1999; 01-JUN-1999;
	999;
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9905-0137528. 9905-0137528. 9905-0137528. 9905-0138094. 9905-0138049. 9905-0139453. 9905-0139453. 9905-0139458. 9905-0139458. 9905-0139458. 9905-0139458. 9905-0139458. 9905-0139458. 9905-0139458. 9905-0139458. 9905-0139461. 9905-0139461. 9905-0139462. 9905-0140534. 9905-0140534. 9905-0140534. 9905-0140534. 9905-014053. 9905-014053. 9905-014053. 9905-014053. 9905-014433. 9905-014433. 9905-014433. 9905-014433. 9905-014433. 9905-014433. 9905-014433. 9905-014433. 9905-014433. 9905-014433. 9905-014433. 9905-014433. 9905-014433. 9905-014433. 9905-014433. 9905-014433. 9905-014459. 9905-014459. 9905-014459. 9905-01459. 9905-01459. 9905-01459. 9905-01459. 9905-01459. 9905-01459. 9905-01459. 9905-01459. 9905-01459.	5629. 6021. 6392. 6782. 7222.
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05-AUG-1999 06-AUG-1999 06-AUG-1999 09-AUG-1999 11-AUG-1999 11-AUG-1999 11-AUG-1999 11-AUG-1999 11-AUG-1999 11-AUG-1999 12-AUG-1999 12-AUG-1999 12-AUG-1999 13-AUG-1999 13-AUG-1999 13-AUG-1999 13-AUG-1999 13-AUG-1999 13-AUG-1999 13-AUG-1999 13-AUG-1999 13-AUG-1999 14-AUG-1999 11-SEP-1999 11-SEP-1999 11-SEP-1999 11-SEP-1999 11-SEP-1999 11-CCT-1999 11-CCT-1999 11-CCT-1999 11-CCT-1999 11-CCT-1999 11-CCT-1999 11-CCT-1999 11-CCT-1999 11-CCT-1999 12-CCT-1999 12-CCT-1999 13-CCT-1999 13-CCT-1999 14-CCT-1999 15-CCT-1999 15-CCT-1999 16-CCT-1999 17-CCT-1999 18-CCT-1999 18-CCT	R 02-AUG-1999; R 03-AUG-1999; R 04-AUG-1999; R 04-AUG-1999; R 04-AUG-1999;
05-AUG-1999 99US 06-AUG-1999 99US 06-AUG-1999 99US 06-AUG-1999 99US 06-AUG-1999 99US 07-AUG-1999 99US 11-AUG-1999 99US 11-AUG-1999 99US 11-AUG-1999 99US 11-AUG-1999 99US 11-AUG-1999 99US 11-AUG-1999 99US 20-AUG-1999 99US 20-AUG-1999 99US 21-AUG-1999 99US 21-AUG	R 02-AUG-1999; 99US R 03-AUG-1999; 99US R 04-AUG-1999; 99US R 04-AUG-1999; 99US R 05-AUG-1999; 99US
05-AUG-1999; 99US-011 06-AUG-1999; 99US-012 06-AUG-1999; 99US-012 09-AUG-1999; 99US-012 10-AUG-1999; 99US-013 11-AUG-1999; 99US-013	R 02-AUG-1999; 99US-010 R 03-AUG-1999; 99US-010 R 04-AUG-1999; 99US-010 R 04-AUG-1999; 99US-010 R 05-AUG-1999; 99US-010
05-AUG-1999; 99US-01 06-AUG-1999; 99US-01 06-AUG-1999; 99US-01 06-AUG-1999; 99US-01 07-AUG-1999; 99US-01 10-AUG-1999; 99US-01 11-AUG-1999; 99US-01 11-AUG-1999; 99US-01 11-AUG-1999; 99US-01 11-AUG-1999; 99US-01 12-AUG-1999; 99US-01 13-AUG-1999; 99US-01 14-AUG-1999; 99US-01 14-AUG-19	R 02-AUG-1999; 99US-010 R 03-AUG-1999; 99US-010 R 04-AUG-1999; 99US-010 R 04-AUG-1999; 99US-010 R 05-AUG-1999; 99US-010
05-AUG-1999; 99US-011 06-AUG-1999; 99US-012 06-AUG-1999; 99US-012 09-AUG-1999; 99US-012 11-AUG-1999; 99US-012 11-AUG-1999; 99US-011 11-AUG-1999; 99US-011 11-AUG-1999; 99US-011 11-AUG-1999; 99US-011 11-AUG-1999; 99US-011 12-AUG-1999; 99US-011 13-AUG-1999; 99US-011 13-AUG-1999; 99US-011 14-AUG-1999; 99US-011	R 02-AUG-1999; 99US-010 R 03-AUG-1999; 99US-010 R 04-AUG-1999; 99US-010 R 04-AUG-1999; 99US-010 R 05-AUG-1999; 99US-010

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Best Local S
Matches 7
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12-JAN-1990;
01-MAR-1990;
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28-OCT-1999;
29-OCT-1999;
              556 del A is a frameshift mutation in exon 4 and results in shortened polypeptides significantly different from the single amino acid deletions or alterations.

The mutant CF gene when expressed in cells of the human body, is associated with altered cell function which correlates with the genetic disease cystic fibrosis.

See also AAQ13053-72.
                                                                                                                     Mutant cystic fibrosis trans-membrane conductance regulator gene - used for producing prods. for diagnosis, screening and therapy of cystic fibrosis
                                                                                                                                                               WPI; 1991-238022/32.
N-PSDB; AAQ13068.
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Sequence
                                                                                                  Claim 20; Page 124; 178pp; English.
                                                                                                                                                                                             Tsui LC, Rommens JM,
                                                                                                                                                                                                                 (HSCR-) HSC RES DEV CORP.
                                                                                                                                                                                                                                                                              11-JAN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deletion; mutant; diagnosis; antibodies;
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70 gailevc 76
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90CA-2007699.
90CA-2011253.
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99US-0162142.
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/note= "by protein kinases C"
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Q923v8 rattus norv
Q9bs64 homo sapien
Q9n4c6 caenorhabdi
Q9alm1 streptococc
Q9vvj7 drosophila
Q9s578 pseudomonas
Q9s578 pseudomonas
Q9yx13 brevibacter
Q96yr9 sulfolobus
Q9syl3 arabidopsis
Q9znx6 rhizobium m
Q9xkn3 anthophora
Q9maz1 glycine max
Q27963 archaeoglob
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ALIGNMENTS

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16 RLLLATVLQAVSAFGAEFSSEACRELGFSSNLLCSSCDLLGQFNLLQLDPDCRGCQEI	Query Match 90.1%; Score 146; DB 4; Length 162; Best Local Similarity 100.0%; Pred. No. 6.6e-142; Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE 162 AA; 17750 MW; 5B94FBB423A089EE CRC64;	EMBL; AF288991; AAG31556.1;	. J. Biol. Chem. 275:35540-35547(2000).		"Structure-Expression Relationships of the 15-kDa Selenoprotein Gene.			Kumaraswamy E. Majukh A. Korotkov K.V. Kozyavkin s	PubMed=10945981:	[2]	, Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.	Pearce A.	SEQUENCE FROM N.A.		NCBI_TaxID=9606;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae	Eukaryota; Me	Homo sapiens (Human).	DJ604K5.1 OR SEP15.	DJ604K5.1 (15 KDA SELENOPROT	01-MAR-2001 (TrEMBLrel. 16, Last	01-MAR-2001 (TrEMBLrel. 16,			Q9GZWO PRELIMINARY; PRT; 162 AA.	09GZW0	RESULT 1

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Kumaraswamy E., Malykh A., Korotkov K.V., Kozyavki Kwon S.Y., Moustafa M.E., Carlson B.A., Berry M.J. Hatfield D.L., Diamond A.M., Gladdyshev V.N.;
"Structure-Expression Relationships of the 15-kDa POSSIBLE ROLE OF THE PROTEIN IN CANCER ETIOLOGY.";
J. Biol. Chem. 275:35540-35547(2000).
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01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
15 KDA SELENOPROTEIN.
                                                                                                                                                   Roethlein D., Kyriakopoulos A., Behne D.;

A 15 kDa-selenoprotein in several tissues of
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ
EMBL; AF390544; AAK73100.1;
SEQUENCE 162 AA; 17706 MW; 65E939968C8B721
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15, KDA CYTOSOLIC SELENOPROTEIN.
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MGD; MGI:1927947;
SEQUENCE 162 AA,
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; NCBI_TaxID=10116;
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
"Genome sequence of the nematode C. investigating biology. The C. elega Science 282:2012-2018(1998).
                                                                  SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE-99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                          NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                     QFETKKLYAGAILEVCG
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BC005294; AAH05294.1;
BC016359; AAH16359.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
77; Conserv
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(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
L 17.6 KDA PROTEIN.
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(TrEMBLrel. 19, Last annotation update)
L 9.7 KDA PROTEIN.
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                                                                     PubMed=9851916;
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100.0%; Pr
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                          The C. elegans Sequen
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                                                                                                                                         Caenorhabditis
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                                                                                                                                                                                                                                                                  PRT;
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Best Local
09VVJ7
09VVJ7;
01-MAY-2000
01-MAY-2000
01-MAY-2000
CG7484 PROTE
CG7484.
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                                                                                                                                                                                                                                                          Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an MI strain of Streptococcus pyogenes."; Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
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01-JUN-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                 Pfam; PF01527; Transposase_8; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 97 AA; 11418 MW; 81F2B17A7D2B60BB CRC64;
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STRAIN-SF370 / ATCC
                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes;
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SEQUENCE 1
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STRAIN-BRISTOL
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nes 9; Conserv
                                                                                                                     64
                                                                                                                                                                       Local Similarity
                                                                                                                    AQFETKKL
                                                                                                                                        AQFETKKL 82
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             PROTEIN.
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                     (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
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                                                                PRELIMINARY;
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) to the EMBL/GenBank/DDBJ
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19,
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Last annotation update)
                                                                                                                                                             Score 8; DB 1; Pred. No. 2.9
0; Mismatches
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                     Last sequence update)
Last annotation update)
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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Hank M.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Hank M.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Hank M.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Hank M.H., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beleson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolishov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolishov S.,
RA Geryd D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Laris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davis P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davis P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davis P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davis P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davis P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davis P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davis P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davis P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davis P.,
RA Glasser K., Gorrell J.H., Gu Z., Mays A.D., Dew I., Dletz S.M.,
RA Glasser K., Gorrell J.H., Gu Z., Gdan P., Harris M.,
RA Glasser K., Gorrell J.H., Gu Z., Gdan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., J.A, Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Juny D.M., Nelson D.L.,
RA Kimmel B.E., Kodira C.D., Kraft C., Scheeler F., Shen H.,
RA Kimmel B.E., Kodira C.D., Kraft C., Scheeler
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Best Local S
Matches 8
                                                                                                                                              Q9S578
Q9S578;
Q1-MAY-2000
Q1-MAY-2000
Q1-DEC-2001
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Eukaryota; Metazoa; Arthropoda; Tracheata; He
Eukaryota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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MEDLINE=20196006; PubMed=10731132;
Annihor S.E., Holt R.A.,
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Amanatides P.G., Scherer S.E., Li P.W.,
                              Bacteria; Proteobacteria;
                                                          Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 LQIKYVRG 123
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                                                                                      2 PROTEIN (P
2 OR PA0618.
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8; Conser
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(TrembLrel.
(TrembLrel.
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                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                     BACTERIOPHAGE
                                                                                                                                              13, Created)13, Last sequence update)19, Last annotation updat
                              gamma
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Pred. No
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                              subdivision; Pseudomonadaceae;
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RESULT
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REPLINE-20437337; PubMed=10984043;

X MEDLINE-20437337; PubMed=10984043;

X MEDLINE-20437337; PubMed=10984043;

XA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Garber R.L., Goltry L., Tolentino E., Weestbrook-Wadman S., Yuan Y.,

RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

opportunistic pathogen.";

RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an

opportunistic pathogen.";

RT Nature 406:959-964(2000).

DR EMBL; AE004498; BAA83156.1; -.

DR EMBL; AE004498; AAG04007.1; -.
                                                                                                       Query Match
Best Local
Matches
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Matches
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SEQUENCE
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STRAIN-ATCC 15692 / PAO1;

Nakayama-K., Takashima K., Ishihara H., Shinomiya T., Kageyama M.,

Nakayama-K., Ohnishi M., Murata T., Terawaki Y., Mori H., Hayashi T.;

"Genetic relationship between bacteriocins and bacteriophages.";

"Genetic relationship between bacteriocins and bacteriophages.";

Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-OCT-2000 (TrEMBLrel. 15, Last annotation
HYPOTHETICAL 40.2 KDA PROTEIN (FRAGMENT).
Bukaryota, Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                              MEDLINE-2015471; PubMed-10693804; Millonig J.H., Millen K.J., Hatten M.E.; "The mouse Dreher gene Lmxla controls for the vertebrate CNS."; Nature 403:764-769(2000).
EMBL; AF226663; AAF43013.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9JKU7
                                                                                                                                                                          Hypothetical protein.
NON_TER 1
SEQUENCE 365 AA; 4
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8; Conser
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295 AA;
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                                                                                                                                                                            86329D3A8BA5C59F CRC64;
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Q96YR9;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TREMBLREL. 1
HYPOTHETICAL PROTEIN ST21
ST2104.
Sulfolobus tokodaii.
Archaea; Crenarchaeota; S
NCBI_TaxID=111955;
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Q9WXI3;
01-NOV-1999
01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN-JCM 10545 / 7;

STRAIN-JCM 10545 / 7;

STRAIN-JCM 10545 / 7;

STRAIN-JCM 10545 / 7;

STRAIN-JCM 1054 / 7;

FubMed=11572479;

Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Kawarabayasi Y., Hino Y., Ankai A., Kosugi H., Hosoyama A., Fukui S., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Sekine M., Nakazawa H., Takamiya M., Kato Y., Nagai Y., Nishizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.;
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SEQUENCE
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Micrococcineae; Brevibacteriaceae; Bre
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                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodali strain7."; DNA Res. 8:123-140(2001). EMBL; AP000988; BAB67208.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.";
Submitted (MAR-1999) to the
EMBL; AB025195; BAA76382.1;
                                                                                                                                                                                                                                                                                             Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal; Hydrolase; Glycosidase
SIGNAL 1 37 P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-0407
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01-NOV-1999 (TrEMBLrel. 12, Last sequence up
01-NOV-1999 (TrEMBLrel. 12, Last annotation
ISOMALTOTRIO-DEXTRANASE PRECUSOR PRECURSOR (
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141 AA; 10
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L PROTEIN ST2104.
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ISOMALTOTRIO-DEXTRANASE.
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                                                                                                                                       DB , 43;
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16;
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                                                                                                                                                                                       Length 141;
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Brevibacterium
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RESULT
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Best Local S
Matches 7
                                               Gallbert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F., Barloy-Hubler F., Finan T.M., Long S.R., Becker A., Boistard P., Bothe G., Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G., Boutry M., Bowser L., Buhrmester J., Cadleu E., Capela D., Chain P., Cowle A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F., Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M., Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D., Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V., Masuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B., Norhoelter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J., "The composite genome of the legume symbiont Sinorhizobium meliloti."; Science 293:668-672(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CV. COLUMBIA;
Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
Federspiel N.A., Palm C.J., Rowley D., Buehler E., Dunn I
Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn I
Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.
Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ACOO7153; AAD30621.1;
InterPro; IPR000345; CYTC_heme_bind.
PROSITE; PS00190; CYTCCHROWE C; UNKNOWN_1.
SEQUENCE 158 AA; 17901 MW; A181CB37D4A33B8B CRC64;
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01-MAY-2000
01-JUN-2001
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID-3702;
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Q9SYL3;
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01-DEC-2001 (TremBLrel. 19, Last sequence update)
01-DEC-2001 (TremBLrel. 19, Last sequence update)
01-DEC-2001 (TremBLrel. 19, Last annotation update)
PUTATIVE RNA POLYMERASE SIGMA FACTOR FECI PROTEIN.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21368234; PubMed=11474104;
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                                   proteome.
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TrEMBLrel.
TremBLrel.
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     18395 MW;
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13,
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Last annotation update)
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Pred. No.
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     CRC64;
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Query Match

Score

7;

DB

16;

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RP SEQUENCE FROM N.A.

RP SEQUENCE S., Schmid-Hempel R., Roubik D., Schmid-Hempel P.;

RT "Relationships within the Apinae.";

RP SEQUENCE (MAY-1997) to the EMBL/GenBank/DDBJ databases.

CC CHUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE

CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A

CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A

CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

CC COPACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY

CC COPACTOR: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,

CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
    RESULT ID PART ID PART
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Matches
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Eukaryota; Metazoa; Ai
Pterygota; Neoptera; I
Apoidea; Apidae; Anth
NCBI_TaxID=60897;
                                                                                                                                                                                                       01-OCT-2000
01-OCT-2000
01-JUN-2001
NONCLATHRIN
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SEQUENCE
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01-DEC-2001
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Electron
SEQUENCE FROM N.A. Hahn Y., Chung J.H.;
                                                                 Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
eurosids I; Fabales; Fabaceae;
CCBI_TaxID=3847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SIMILARITY: BELONGS TO THE EMBL; AF002731; AAD29081.1; -InterPro; IPR000179; Cyt.b_b6.
Pfam; PF00033; Cytochrome_b_N;
                                                                                                                                                             Glycine max (Soybean).
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Neoptera; Endopterygota; Hymenoptera; Apocrita; Ac
pidae; Anthophora.
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173
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(TrEMBLrel. 15, Last sequence update)
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COAT PROTEIN ZETA2-COP.
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                                                                                            Fabaceae;
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RT "Identification of zeta-COP genes from various organisms.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

DR EMBL, ABO40543; BAA93004.1; -.

DR InterPro; IPR000804; Clat_adaptor_s.

DR Pfam; PF01217; Clat_adaptor_s: 1.

KW Coat protein.

SQ SEQUENCE 179 AA; 19790 MW; CC01CFE2EB84341C CRC64;

Ouery Match
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LATVLQA 25

[11111]
Db 90 LATVLQA 96

Search completed: September 18, 2002, 16:38:58

Job time: 213 sec
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Minimum DB Maximum DB Title: Perfect score: Total number of hits satisfying chosen parameters: Word size : Searched: Scoring table: Sequence: Run on: OM protein - protein search, using sw model seq length: 0 length: 2000000000 US-09-676-718A-1 162 1 MAAGPSGCLVPAFG 0 283138 seqs, 96089334 residues OLIGO Gapop 60.0 , Gapext 60.0 September 18, GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd MAAGPSGCLVPAFGKRLLLA.....ILKWNTDSVEEFLSEKLERI 162 2002, 16:33:55; Search time 18.81 Seconds (without alignments) 827.564 Million cell updates/sec 283138

Post-processing: Listing first 45 summaries

Database :

pir1:*
pir2:*
pir3:*
pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	G	4	ω	N	_	NO.	Requil+
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porphobilinogen sy	alpha-l-antitrypsi	1-deoxy-D-xylulose	acetylornithine de	transcription init		hypothetical prote	nonstructural prot	leucoanthocyanidin	probable pectinest	hypothetical prote	probable membrane	cal p	S. aureus Cbf1 pro	reductase BH1493 [rRNA methylase (AP	rRNA methylase [im	υı		hypothetical prote	conserved hypothet	T-cell surface gly		alpha-amylase inhi	probable allophyco	phosphoenolpyruvat	phosphoribosylform	м	hypothetical prote	Description	

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hypothetical prote hypothetical prote		dnak protein [impo	hypothetical prote	N-acetylgalactosam exopolyphosphatase	hypothetical prote conserved hypothet	NADH oxidase (nox) probable polygalac	hypothetical prote

ALIGNMENTS

C;Genetics: A;Gene: PA0618 A;Note: JR2 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-295 <STO>
A;Cross-references: GB:AE004498; GB:AE004091; NID:g9946491; PIDN:AAG04007.1; GSPDB:GN
A;Experimental source: strain PAO1 C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 31-Dec-2000 C;Accession: T44541; H83566
C;Accession: T44541; H83566
C;Accession: T44541; H83566
C;Accession: T46541; H83566
C;Accessio hypothetical protein JR2 [imported] - Pseudomonas aeruginosa N;Alternate names: probable bacteriophage protein PA0618 C;Species: Pseudomonas aeruginosa A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A;Reference number: A82950; MUID:20437337
A;Accession: H83566 A;Cross-references: EMBL:AB030825; PIDN:BAA83156.1
A;Experimental source: strain PAO1
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-295 <NAK> A; Reference number: A; Accession: T44541

рa

dextranase (EC 3.2.1.11) - Brevibacterium fuscum var. dextranlyticum N;Alternate names: isomaltotrio-dextranase C;Species: Brevibacterium fuscum var. dextranlyticum C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000 C;Accession: JC7142; PC7042 R;Mizuno, T.; Mori, H.; Ito, H.; Matsui, H.; Kimura, A.; Chiba, S. Brock Bideroka, Brock Bideroka RESULT JC7142 Ş 밁 Query Match
Best Local Similarity
Matches 8; Conserv 124 SDPVLKLL 131 44 SDPVLKLL 51 Conservative H.; Ito, Biochem. 4.9%; Score 8; 1 100.0%; Pred. No. H.; Matsui, H.; Kimura, A.; Chiba, S. 63, 1582-1588, 1999 0; Mismatches DB 2; 0, Length 295; Indels 0; Gaps

0

Biotechnol.

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C;Accession: AE0478
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davie, P.; Dougan, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barra Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Molecular cloning of isomaltotrio-dextranase A;Reference number: JC7142; MUID:20008261
A;Accession: JC7142
A;Molecule type: DNA
A;Residues: 1-641 <MII>
A;Experimental source: Strain 0407
A;Accession: PC7042
A;Accession: PC7042
                                                       A; Reference number: AB0001;
A; Accession: AE0478
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-878 < KUR>
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 A;Cross-references:
C;Genetics:
A;Gene: ppc
                                                                                                                                                                                                                                                 phosphoenolpyruvate carboxylase (EC 4.1.1.31) [imported] - Yersinia pestis (strain C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Accession: AE0478
                                                                                                                              A; Title: Genome sequence of Yersinia pestis, the causative A; Reference number: AB0001; MUID:21470413; PMID:11586360
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A; Residues: 1-743 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, Nucleic Acids Res. 28, 4317-4331, 2000
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C;Keywords: glycosidase;
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| 119 GAEFSSEA 126
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nes 8; Conserv
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                                   PID:g15981839;
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RESULT
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A;Cross-references: EMBL:X17575; NID:g21700; PIDN:CAA3:C;Superfamily: wheat alpha-amylase inhibitor C;Keywords: alpha-amylase inhibitor; tetramer F;1-25/Domain: signal sequence #status predicted <SIG>F;26-145/Product: alpha-amylase inhibitor chain CM1 #s
                                                                                                                                                                                                                                                                                         C;Accession: Sluuz,
C;Accession: Sluuz,
R;Garcia-Maroto, F; Marana, C;
plant Mol. Biol. 14, 845-853, 199
                                                                                                                                                                                                                                                                                                                                                alpha-amylase inhibitor, tetrameric, chain CMl precursor - wheat C;Species: Triticum aestivum (common wheat)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Mol. Biol. 20, 267-276, 1992
A;Title: Organization and expression of a
A;Reference number: S25306; MUID:93004479
A;Accession: S25307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable allophycocyanin linker protein - red alga
C;Species: chloroplast Cyanidium caldarium
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Genome: chloroplast
C;Superfamily: probable allophycocyanin linker protein
C;Keywords: chloroplast
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                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-145 <GAR>
                                                                                                                                                                                                                                                       A; Reference number: S10027; MUID:91346675
A; Accession: S10027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-83 <VAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Valentin, K.; Maid, U.; Emich, A Plant Mol. Biol. 20, 267-276, 1992
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10 LLLATVL
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                                                            Score 7; DB 2; Pred. No. 22; 0; Mismatches
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conserved hypothetical protein AF2321 - Archaeoglobus fulgidus (;Species: Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Date: 05:Dec:1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999 C;Accession: A69540 R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodsor R;Klenk, H.P.; Clayton, R.A.; Tomb, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weldman, J.F.; McDonald, L. Nature 390, 364-370, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-173 <LDNA
A;Residues: 1-173 <LDNA
A;Cross-references: EMBL:X53430; NID:955913; PIDN:CAA37521.1; PID:955914
C;Superfamily: T-cell surface glycoprotein CD3 delta chain; immunoglobulin homology
C;Reywords: glycoprotein; transmembrane protein
C;Reywords: glycoprotein; transmembrane protein
F;30-75/Domain: immunoglobulin homology <IMM>
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A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Lin, S.X.; Liu, S.A.; Luros, J.S.; Maiti, R.; Marziali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Accession: E86191

A;Accession: E86191
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A69540
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Nucleic Acids Res. 18, 4617, 1990
A;Title: Nucleotide sequence of a cDNA encoding the rat T3 delta chain.
A;Reference number: S10975; MUID:90356424
A;Accession: S10975
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C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: E86191
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C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S10975
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A;Map position: 1
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A;Residues: 1-158 <STO>
A;Cross references: GB:AE005172;
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Sykes,
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A;Status: Lau....A;Status: Lau....A;Anolecule type: DNA
A;Rolecule type: DNA
A;Residues: 1-196 <KAL>
A;Cross-references: EMBL:AF075597; NID:g3298610; PID:g3377809
A;Cross-imental source: cultivar Columbia
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A; Introns: 77/1
A; Note: T2H3.15
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submitted to the EMBL Data Library, August
A;Description: The sequence of A. thaliana
A;Reference number: Z14324
A;Accession: T01425
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                                                                                                                                                                          A; Reference number: Z20273
                                                                                                                                                                                                                                  hypothetical protein Y43C5B.1 - Caenorhabditis elegans (fragment) C;Species: Caenorhabditis elegans C;Species: C-coct-1999 #sequence_revision 15-Oct-1999 #text_change 1 C;Accession: T26829
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A; Map position:
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A; Residues: 1-197 <WIL>
                                                                                                                               A; Status: preliminary; translated from GB/EMBL/DDBJ
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A; Accession: T26829
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                  A; Gene: CESP:Y43C5B.1
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                                                                            GSPDB:GN00022; CESP:Y43C5B.1
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Query Match Best Local S Matches 7

Similarity 7; Conserv

4.3%; Score 7; DB 2 ilarity 100.0%; Pred. No. 29; Conservative 0; Mismatches

2

0;

Indels

0

Gaps

0

Length 197;

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TRNA methylase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C;Accession: AE2618
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, 1 erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                    Query Match
Best Local Similarity
Them 7; Conserv
                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE008688; PIDN:AAL41363.1; PID:g17738678; GSPDB:GN00186 A;Experimental source: strain C58 (Dupont) C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
A; Gene: Y43C5B.1
A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Rote: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: C88809
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                                                                                                                                                                                                                                           A; Map position: circular C; Superfamily: conserved
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A; Residues: 1-282 <KUR>
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A; Residues: 1-197 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein Y43C5B.1 [imported] - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
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:Accession: C88809
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A;Molecule type: DNA
A;Residues: 1-298 <5TO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reductase BH1493 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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                                                                                                                                                                                                                                                                                                                               A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BAB05212.1; A;Experimental source: strain C-125
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A; Residues: 1-290 < KUR>
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                                                                                                                                            Mismatches
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OM protein - protein search, using sw model GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

September 18, 2002, 16:36:11; Search time 10.7 Seconds (without alignments) 586.221 Million cell updates/sec

Title: Perfect score: Sequence:

Run on:

US-09-676-718A-1 162 1 MAAGPSGCLVPAFGKRLLLA......ILKWNTDSVEEFLSEKLERI 162

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: Word size :

105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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P42127	208888	078492	P79407	203288	P11375	004421	P95990	P48138	P94425	P05868	P45905
homo sapier	buchnera ap	guillardi	vulpes vu	mus muscu	equus asi	arabidops	sulfolobus	cyanophor	bacillus su	human immu	bacillus :

ALIGNMENTS

88888888	CCCCR88888	RA RA RA	RA RA RA	R R R R R R R R R R R R R R R R R R R	RESULT SE15_H ID S AC ODT DT 1 DT 1 DT 1 C OC O
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE-Bone marrow, and Kidney; Strausberg R.; Strausberg R.; Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases. -!- SUBUNIT: SEEMS TO BE EITHER OLIGOMERIC OR HETEROOLIGOMERIC. -!- PTM: THE N-TERMINUS IS BLOCKED. -!- MASS SPECTROMETRY: MW-14870; METHOD-Electrospray; RANGE-?-152.	RYU M., MOON E.; RYU M., MOON E.; "The human 15-kDa selenoprotein gene: characterisation of the genomic structure and functional analysis of the promoter."; submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. [4] SEQUENCE FROM N.A. Pearce A.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. KOTOKLOV K.V., KOZYAVKIN S., Hu Y., KUMARASWAMY E., MALYKH A., KOTOKLOV K.V., KOZYAVKIN S., Hu Y., KWON S.Y., MOUSTAFA M.E., CARLSON B.A., Berry M.J., Lee B.J., HATFIELD D.L., Diamond A.M., Gladyshev V.N.; "Structure-expression relationships of the 15-kDa selenoprotein gene. Possible role of the protein in cancer etiology."; J. Biol. Chem. 275:35540-35547(2000).	[1] [1] [1] [1] SEQUENCE FROM N.A., AND SEQUENCE OF 98-106; 123-127 AND 146-158. MEDIJINE-98204881; PubMed-9535873; Gladyshev V.N., Jeang KT., Wootton J.C., Hatfield D.L.; "A new human selenium-containing protein. Purification, characterization, and cDNA sequence."; J. Biol. Chem. 273:8910-8915(1998).	LT 1 _HUMAN STANDARD; PRT; 162 AA. SE15_HUMAN STANDARD; PRT; 162 AA. O60613; O9NRO1; Q9BS64; O9GZWO; 15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) O1-MAR-2002 (Rel. 41, Last annotation update) O1-MAR - 2002 (Rel. 41, Last annotation update) 15 kDa selemoprotein precursor. 15 kDa selemoprotein precursor. SEP15. HOmo sapiens (Human). HOmo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCHI Taylogofo.

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RESULT 2
SE15_MOUSE
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15 kDa selend
                                                                                                                  This SWISS-PROF entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                      MEDILINE=20519655; PubMed=10945981; Kumaraswamy E., Malykh A., Korotkov K.V., Kozyavkin S., Hu Y., Kwon S.Y., Moustafa M.E., Carlson B.A., Barry M.J., Lee B.J., Hatfield D.L., Diamond A.M., Gladyshev V.N.; "Structure-expression relationships of the 15-kDa selenoprotein Possible role of the protein in cancer etiology."; J. Biol. Chem. 275:35540-35547(2000).
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EMBL;
EMBL;
EMBL;
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EMBL;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MIM; 606254;
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AF288991;
AF267986;
AF267982;
AF267983;
AF267984;
AF267984;
AF267989;
BC005294;
                                                                                              AF288740; AAG31765.1; ALT_SEQ.
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2; AAG31556.1; -.
2; AAG31557.1; -.
2; AAF78966.1; JOINED.
3; AAF78966.1; JOINED.
4; AAF78966.1; JOINED.
5; AAF78966.1; JOINED.
6; CACO4186.1; ALT_TERM.
6; AAH65294.1; ALT_TERM.
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    Last sequence update)
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162
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Pred. No
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15 KDA SELENOPROTEIN.
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0923V8;
01-MAR-2002 (Rel. 41,
01-MAR-2002 (Rel. 41,
01-MAR-2002 (Rel. 41,
15 kDa selenoprotein p
                                                       DEXT_ARTGO STANDARD; PRT; 640 AA. P70744; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) Dextranase precursor (EC 3.2.1.11) (Alpha-1,6-9lucanohydrolase) (Endodextranase). Arthrobacter globiformis.
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SE_CYS
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roethlein D., Kyriakopoulos A., Behne D.;
"A 15 kDa-selenoprotein in several tissues of
"A 15 kDa-selenoprotein in several tissues of
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                        ARTGO
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Mammalia; Eutheria;
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              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Micrococcineae; Micrococcaceae; Arthro
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59; Conservative
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162 AA; 17775 1
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Rodentia;
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thes 0;
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8.6e-63;
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                     Arthrobacter.
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                                                                                                     Bacillus halodurans.
Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oguma T., Kurokawa T., Tobe K., Kitao S., Kobayashi M.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,6-alpha-D-glucosidic
                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                         STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Phosphoribosylformylglycinamidine synthase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PURL_BACHD Q9KF57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.
STRAIN-T-3044;
                                                                                                                                                                                                                                         Horikoshi K.;
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                                                                                                                                                                                                                                                               Takami H.,
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nes 8; Conserv
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SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO FAMILY 49 OF GLYCOSYL HYDROLASES.
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71142 MW;
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DEXTRANASE.
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RESULT 7
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YC20_GALSU
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01-AUG-1990
01-AUG-1990
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01-FEB-1996
01-FEB-1996
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Valentin K., Maid U., Emich A., Zetsche K.;
"Organization and expression of a phycobiliprotein gene cluster from
the unicellular red alga Cyanidium caldarium.";
Plant Mol. Biol. 20:267-276(1992).
-I- SIMILARITY: BELONGS TO THE YCF20 FAMILY.
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STRAIN=14-1-1 / ISOLATE 107.79/GOETTINGEN;
MEDLINE=93004479; PubMed=1391770;
MEDLINE=93004479; PubMed=139170;
MEDLINE=93004479; PubMed=139170; PubMed=13
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InterPro; IPR000728; AIRS_related.
Pfam; PF00586; AIRS; 2.
Pfam; PF02769; AIRS_C; 2.
Purine biosynthesis; Ligase; ATP-binding; Complete proteome.
NP_BIND 111 122 ATP (POTENTIAL).
SEQUENCE 743 AA; 80008 MW; 005FC0855D20D84D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; x57251; CAA40532.1; -.
PIR; S25307; S25307.
Chloroplast; Hypothetical protein.
SEQUENCE 83 AA; 9485 MW; 990117EC63FF3EF9 CRC64;
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Pred. No.
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SEQUENCE
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PIR; S10027; S10027.
HSSP; P01087, 1B10.
InterPro; IPR003612; AAI.
InterPro; IPR001768; Cereal_tryp_amyl_inh.
Pfam; PF00234; tryp_alpha_amyl; 1.
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Spermatophyta; Magnoliophyta;
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STRAIN-CV. CHINESE SPRING;
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SIMILARITY: BELONGS TO THE CEREAL TRYPSIN/ALPHA-AMYLASE INHIBITOR FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: ALPHA-AMYLASE/TRYPSIN IN INSECT DEFENSE MECHANISMS.
                                                                                                                               LLLATVL
                                                                                                                                                                                                                                                                                                                  Signal.
                                                                                                                                                                                                                                                                                                                                                  ; PR00808; ÂMLASĒINHBTR.
SM00499; AAI; 1.
E; PS00426; CEREAL_TRYP_
                                                                                                                                                                                                                                                                                                                                    protease inhibitor;
                                                                                                                                                                                         Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    non-profit institu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biophys. Acta 873:147-151(1986)
                                                                                                                                                                                                                                                                      26
145 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        equires a license agreement (See email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CANDEAL
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   (Rel. 40, (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; CAA35598.1;
; A25310.
; S10027.
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT OF THE TETRAMERIC PECIFICITY: ENDOSPERM.
                                                                                                                               16
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                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14:845-853(1990).
                                                                                                                                                                                                                                                                                                                                CEREAL_TRYP_AMYL_INH; 1. nhibitor; Alpha-amylase 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marana C., Mena M., Garcia-Olmedo F., Carbonero P.; and chromosomal location of genes encoding the three of the wheat tetrameric inhibitor of insect alpha-
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15517
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yta; Lillopsida; Poales; Poaceae; Pooidea
   sequence
                                                                                                                                                                                        Score 7; DB 1
Pred. No. 9.1
0; Mismatches
                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                  ALPHA-AMYLASE/TRYPSIN INHIBITOR 119EDBD8C1229672 CRC64;
                                                PRT;
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                                                165
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. 9.1;
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                                                                                                                                                                                                                                                                                                                                  inhibitor; Multigene
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Matches
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Best Local
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P19377;
01-NOV-1990
01-NOV-1990
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or send a
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Barsyte D., Tipping D., Brennand J., Haker B., LOVEJOY L., "Cloning of rainbow trout urotensin I.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: UROTENSIN IS FOUND IN THE TELEOST CAUDAL NEURO SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS CORTICOTROPIN-RELEASING FACTOR. THE NONHORMONAL PORTION PRECURSOR MAY BE A UROTENSIN BINDING PROTEIN, UROPHYSIN.
 SEQUENCE FROM N.A.
STRAIN=WISTAR;
MEDLINE=90356424; PubMed=2143819;
Davies J.D., Mueller D., Wilson D.B.,
"Nucleotide sequence of a cDNA encodi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oncorhynchus mykiss (Rainbow trout)
Eukaryota; Metazoa; Chordata; Cranial
Actinopterygii; Neopterygii; Teleost
Protacanthopterygii; Salmoniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rea.
                                                                                                        NCBI_TaxID=10116;
                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                             Rattus norvegicus
                                                                                                                                                                                                             T-cell surface glycoprotein
                                                                                                                                                                                                                              01-NOV-1990 (Rel.
01-NOV-1990 (Rel.
01-MAR-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ005264; CAA06461.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Hypothalamus;
Barsyte D., Tipping D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Urotensin I p
Oncorhynchus
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InterPro; IPR003620; Urocortin_CRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                           17 LLLATVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ifiled and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FACTOR/UROTENSIN I FAMILY OF PEPTIDES.
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)a; Chordata;
[a; Rodentia;
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16, Last sequence update)
41, Last annotation updat
41, Cast annotation delta chain
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Sciurognathi; Muridae;
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Best Local
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SEQUENCE FROM N.A.
MEDLINE=21438013; PubMed=11535828;
MEDLINE=21438013; PubMed=11535828;
Jennings C.V., West J., Waine C., Craik D.J., Anderson M.A.;
Blosynthesis and insecticidal properties of plant cyclotides:
Cyclic knotted proteins from Oldenlandia affinis.",
Cyclic knotted proteins from 0ldenlandia affinis.",
                                                                                                                                                                                                                                                                                                                                                                                                                                      P58454;
01-MAR-2002
01-MAR-2002
01-MAR-2002
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TRANSMEM
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OAK4.
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-!- FUNC
-!- SUBU
SEQUENCE OF KALATA B2.

MEDLINE=20069951; PubMed=10600388;

Craik D.J., Daly N.L., Bond T., Waine C.;

"Plant cyclotides: a unique family of cyclic defines the cyclic cystine knot structural mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
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FUNCTION: THE CD3 COMPLEX MEDIATES SIGNAL TRANSDUCTION.

SUBUNIT: THE TCR/CD3 COMPLEX OF T LYMPHOCYTES CONSISTS OF EITHER A TCR ALPHA/BETA OR TCR GAMMA/DELTA HETERODIMER COEXPRESSED AT TI CELL SURFACE WITH THE INVARIANT SUBUNITS OF CD3 LABELED GAMMA, DELTA, EPSILON, ZETA, AND ETA.

SUBCELLULAR LOCATION: Type I membrane protein.

SUBCELLULAR LOCATION: TYPE INVANIOGLOBULIN SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBI European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLLATVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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2 (Rel. 41,
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CHAIN.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

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N-LINKED (GLCNAC. . ) (POTENTIAL).
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RESULT 11
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                            01-OCT-1994 (Rel.
01-OCT-1994 (Rel.
Hypothetical 36.0
                                                                                                                                                                            Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                       MEDLINE=93220397; PubMed=8465606; Doignon F., Biteau N., Crouzet M.
                                                                                                                           STRAIN-S288C;
                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                         NCBI_TaxID=4932;
                                                                                                                                                                    Saccharomycetales;
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                                                                                                                                                                                                                                                               B9K_YEAST
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                                                                                                                                                                                                                                                                                                                                    28 AFGAEFS
                                                            gnon F., Biteau N., Crouzet M., Aigle M.;
e complete sequence of a 19,482 bp segment located
of chromosome II from Saccharomyces cerevisiae.";
st 9:189-199(1993).
SUBCELLULAR LOCATION: Integral membrane protein (P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: Kalata B2 is a cyclic peptide.
SIMILARITY: BELONGS TO THE CYCLOTIDE FAMILY.
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PTM: Kalata B2 is a cyclic pepti
                                                                                                                                                                                                                                                                                                                  AFGAEFS
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Ascomycota; Saccharomycotina; Saccharomycetes;
; Saccharomycetaceae; Saccharomyces.
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VNS2_AHSV9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNS2_AHSV9
P27279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         three different orbiviruses.";
Virology 185:500-504(1991).
-!- FUNCTION: SSRNA-BINDING PROTEIN.
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Hypothetical protein; Transmembrane. Transmem 162 182

TRANSMEM 255 275

TRANSMEM 250 300

SEQUENCE 320 AA; 35986 MW; C5F3H
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EMBL;
PIR;
    RPSD_ANASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE=92024120; PubMed=1656603; van Staden V., Theron J., Greyling B.J., I have a comparison of the nucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an
                                                                                                                                                                                                                                                                                                                                   Nonstructural protein; RNA-binding.
SEQUENCE 365 AA; 41193 MW; 45F3A78754887741 CRC64;
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PIR; A40788; MNXRAH
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    STANDARD;
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tein NS2.
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NS2 gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes
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MBL outstation -
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  DXR_XYLFA
ID DXR_X
AC Q9PEI
DT 16-OC
DT 16-OC
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                                                                                                                     RESULT
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Best Local S
Matches 7
DXR_XYLFA
Q9PEIO;
16-OCT-2001
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                DNA_BIND
                                                                                                                                                                                          120 LSEKLER
                                                                                                                                                                                                                                      155 LSEKLER
(Rel. 40, (Rel. 40,
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SEQUENCE FROM N.A.

MEDLINE=21595285; PubMed=11759840;

Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.

Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

Yasuda M., Tabata S.;

"Complete genomic sequence of the filamentous nitrogen-fixing"

"Complete genomic sequence of the filamentous nitrogen-fixing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DÑA Res. 8:205-213(2001).

-I- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES ANI THEN IS RELEASED. THIS IS THE PRIMARY SIGMA-FACTOR OF THIS
                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000943; Sigma_70.

Pfam; PF00140; Sigma70; 1.

PRINTS; PR00046; SIGMA70FCT.

PROSITE; PS00715; SIGMA70_1; 1.

PROSITE; PS00716; SIGMA70_2; 1.

PROSITE; PS00716; SIGMA70_2; 1.

PROSITE; PS00716; SIGMA70_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brahamsha B., Haselkorn R.;
"Isolation and characterization of the g
sigma factor of the vegetative cell RNA
cyanobacterium Anabaena sp. strain PCC 7
J. Bacteriol. 173:2442-2450(1991).
                                                                                                                                                                                                                                                                                                                                                    DNA-binding; Complete proteome.
DOMAIN 182 195 PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M60046; AAA22043.1; -
EMBL; AD003599; BAB76962.1;
PIR; A42724; A42774.
HSSP; P00579; 1SIG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=91193199; PubMed=1901566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anabaena sp. (strain PCC Bacteria; Cyanobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Encurpean Bioinformatics Institute. There are no resta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE SIGMA-70 FACTOR FAMILY.
                                                                                                                                                                                              7; Conserv
                                                                                                                                                                                                                                                                                                         351
390 AA;
                                                                                                                                                                                                 Conservative
                                                                                                             126
                                                                                                                                                        161
  STANDARD;
                                                                                                                                                                                                                                                                                                                                  370
                                                                                                                                                                                                                                                                                                           45641 MW;
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                                                                                                                                                                                                                                            4.3%;
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                                                                                                                                                                                              %; Score 7; DB 1
%; Pred. No. 23;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ٠.
                                                                                                                                                                                                                                                                                                         POLYMERASE CORE BINDING (POTENTIAL).
H-T-H MOTIF (BY SIMILARITY).
; 604814660815284D CRC64;
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Sigma-A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nostocaceae;
396 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
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                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                          Length 390;
                                                                                                                                                                                                 Indels
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MBL outstation -
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STEER BREEF 
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RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Colanto M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colanto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa -Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Farga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Farga J.S., Lemos M.E., Lopes S.A., Lopes C.R., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.E., Lopes S.A., Lopes C.R., Machado J.A.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Marino C.L.,
Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Manna A. Jr., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Manni A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA Manni A. Jr., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.P.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA Vallada H., Van Silvs M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Silvs M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Silvs M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Silvs M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Silvs M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Silvs M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Van Silvs M.A., Verjovski-Almeida S.M., Tsuhako M.H.,
RA Vallada H., Van Silvs M.A., Verjovski-Almeida S., Vettore A.L.,
RA C. - Colon M.A., Salvs M.A., Verjovski-Almeida S., Vettore A.L.,
RA C. - Colon M.A., Salvs M.A., Verjovsk
밁
                                                                                                                                                                    Query Match
Best Local
                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                        EMBL; AE003942; AAF83858.1; -.
InterPro; IPR003821; DXP_reductoisomerase.
Pfam; PF02670; DXP_reductoisom; 1.
Isoprene blosynthesis; Oxidoreductase; NADP; (POTENTIAL)
NP_BIND
11
18
NADPH (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         step.
-i- SIMILARITY: BELONGS TO THE DXR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-9A5C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (Rel. 41, Last annotation update)
1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267) (DXP
reductoisomerase) (1-deoxyxylulose-5-phosphate reductoisomerase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20365717; PubMed-10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xylella fastidiosa
121
                                                              14

    1-deoxy-D-xylulose 5-phosphate + NADPH.
    PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; second

                                                                     GKRLLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                    Similarity
                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                              42076
                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                  MW;
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                                                                                                                                   o,
                                                                                                                                                                    Score 7;
                                                                                                                                                                                                                                                                                                              14B56FE95748FD97 CRC64;
                                                                                                                                      Mismatches
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                                                                                                                                                                DB 1;
o. 23;
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                                                                                                                                   0
                                                                                                                                                                                                        Length 396;
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                                                                                                                                   Indels
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RESULT 15

RESULT 15

ALAT_MUSCA
ID ALAT_M
AC P26595
DT 01-AUG
DT 01-FEB
DE POTO161
OS ALBAD
OC Mammal
OX MUS CA
OC MAMMAL
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Best Local S
Matches 7
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or send a
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01-AUG-1992 (Rel. 23, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Alpha-1-antiproteinase precursor (Alpha-1-antitrypsin) (Alpha-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Latimer J.J., Berger F.G., Baumann H.; "Highly conserved upstream regions of the alpha 1-atwo mouse species govern liver-specific expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=90136592; PubMed=1689000;
                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                           SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P01009; 9API
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M33567; AAA37128.1; PIR; A34730; ITMSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mechanisms."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus caroli (Wild mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteinase inhibitor) (AAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P26595;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10089;
                                                                                                                                                                                                                                                                                                                             ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000215;
368
                                         20 ATVLQAV 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Extracellular.
TISSUE SPECIFICITY: EXPRESSED NOT ONLY
TUBULE CELLS, WHERE IT IS REGULATED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: INH:
ELASTASE, BUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE SERPIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THROMBIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENT
ATVLOAV 374
                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00079; Serpin; SM00093; SERPIN
                                                                                     Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                          PS00284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. 10:760-769(1990).
ON: INHIBITOR OF SERINE PROTEASES. ITS |
SE, BUT IT ALSO HAS A MODERATE AFFINITY
                                                                                                                                                                                                        25
376
100
133
264
313
412
                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  SERPIN; 1.
; SERPIN; 1.
                                                                                                                                                                                                          3
                                                                                                                                                                                                                                                                                                                                                                                               protease
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377
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                                                                                                             4.3%;
                                                                                                                                                                                                             45872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serpin
                                                                                                                                                                                                                                                                                                                                                                                                 inhibitor; Glycoprotein; Plasma; Signal
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                                                                                                                                                                                                          MW;
                                                                                                                                                                                                     ALPHA-1-ANTIPROTEINASE.
REACTIVE BOND (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                     Score 7; DB 1; Pred. No. 24; 0; Mismatches
                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                    DB
24;
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BY ANDROGENS DURING
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Search completed: September 18, 2002, 16:39:30 Job time: 199 sec

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Minimum DB :
Maximum DB :
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No.
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Perfect score:
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1: /cgn2_6/ptodata/2
2: //gn2_6/ptodata/2
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Match
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162
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
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           US-08-602-359A-34
US-08-871-26R8-23
US-08-871-267B-31
US-09-618-419-31
US-09-163-674-23
US-08-701-651-6
US-08-701-671-2
US-08-701-71-2
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Sequence 34, Appl
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ALIGNMENTS

; MOLECULE TYPE: PROTEIN US-08-602-359A-34	3Y: LIN	AMINO ACID		. ORDITANCE CHARACTERITOR:	: 619-678-5099	Ħ	INFORMATIC	KET NUMBE	TRATION NUMBE	HAILE,	ATTORNEY/AGENT INFORMATION:			; CLASSIFICATION: 435	æ	; APPLICATION NUMBER: US/08/602,359A	LICATION DATA:	WORD PER	SYSTEM:	BM PS/2	TYPE: 3	띩	0	•	•	LA JOLLA	225 EXECU	ADDRESSEE: FISH & RICHARDSON D C	· CODDECTON OF SECONICES . 46	TNATALION: E	CANT: KOSMOTKA,	WARREN, Patrick	SWANSON, Ronald	: LINK, Steven	MAFFI		MURPHY, Dennis		GENERAL INFORMATION:	; bequence 34, Application US/UB6UZ359A ; Patent No. 5942430	US-08-602-359A-34	RESULT 1
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US-08-871-268A-23

; Sequence 23, Application US/08871268A

; Patent No. 5866391
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; MOLECULE TYPE:
US-08-871-268A-23
                                                                                                                                                         US-08-871-267B-31
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Best Local Similarity
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Best Local Similarity
                                                                                                                      Sequence 31, Application US/08871267B Patent No. 6100057
                                                                                                                                                                                                                                                                                        Matches
                                                           GENERAL INFORMATION:
APPLICANT: Elrod, Susan L.
APPLICANT: Cherry, Joel R.
APPLICANT: Jones, Aubrey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212-878-9655 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 48(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,268A
                TITLE OF INVENTION: A Method for Increasing Hemopro'TITLE OF INVENTION: Production in Filamentous Fungi NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias
REGISTRATION NUMBER: 33,
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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CORRESPONDENCE ADDRESS
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APPLICANT: Cherry, Joel R.
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CITY: New York
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405 Lexington Avenue
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100.0%; Pred. No.
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Patent No. 6261827
GENERAL INFORMATION:
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Best Local Similarity
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NAME: ROZEK, CATOL E.
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 4771
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-878-9652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 LGFSSNL
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
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                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/618,419
FILING DATE: 18-Jul-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                   COUNTRY: USA ZIP: 10174 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Elrod, Susan L.
Cherry, Joel R.
Jones, Aubrey
APPLICATION NUMBER: 08/871,267
FILING DATE: 9-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: ROZEK, CATOL E.
                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: A Method for Increasing Hemoprotein Production in Filamentous Fungi
                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                          CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                            ADDRESSEE: No. 62618270 No. 6261827disk Of No. 6261827th America, STREET: 405 Lexington Avenue - 64th Fl.
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5 Lexington Avenue – 64th Fl.
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100.0%; Pred. No.
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; TOPOLOGY: 1; MOLECULE TYPE: US-09-163-674-23
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               Query Match
Best Local Similarity
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Patent No. 6306630
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Best Local :
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APPLICANT: Jones,
APPLICANT: Cherry
                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO: 31:
                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 480
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 63066300 No. 6306630disk of No. 6306630th America,
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TITLE OF INVENTION: Aspergillus Porphobilinogen Synthases
TITLE OF INVENTION: and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                             FILING DATE: 3
CLASSIFICATION:
                                                                                                                                          TYPE:
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nes 7; Conserv
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LENGTH: 424 amino acids
TYPE: amino acid
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REFERENCE/DOCKET NUMBER: 4771.200-US
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                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/255,670A
FILING DATE: 09-JUN-1994
CLASSIFICATION: 435
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SEQ ID NO 6
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CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
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APPLICANT: LOWE, JOHN B
APPLICANT: SMITH, PETER L
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              ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5691180man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2363-
TELECOMMUNICATION INFORMATION:
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25 LGFSSNL 31
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STATE: Virginia
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(703) 413-3000
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o. 44;
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RESULT 9
US-08-812-979-2
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Sheppard, David N.
TITLE OF INVENTION: NOVEL GENES AND PROTEINS FOR TREATING
TITLE OF INVENTION: CYSTIC FIBROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
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LENGTH: 510 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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NAME: Arnold, Beth E.
NAME: 35,430
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100.0%; Pr
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100.0%; Pred. No. 44;
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                                                                    SEQ ID NO 2
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                                                                                                                                                                             APPLICANT: Dong, Jian-yun
APPLICANT: Kan, Yuet Wai
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Efficient AAV Vectors
FILE REFERENCE: 023070-084910US
                                                                                    SOFTWARE:
                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                  PRIOR FILING DATE:
                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/256,703
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INFORMATION FOR SEQ ID NO:
                                                                                                                                 PRIOR APPLICATION NUMBER:
ORGANISM: Homo sapiens OTHER INFORMATION: truncated cystic fibrosis transmembrane
                                      TYPE: PRT
                                                    LENGTH: 1476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 836 amino acid
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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APPLICANT: Sheppard,
TITLE OF INVENTION: N
TITLE OF INVENTION: C
                                                                                                                                                                                                                                                                                                                                                                                           155 LSEKLER 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2, Application US/08812979
o. 5958893
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                                                                                    PatentIn
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SYSTEM: PC-DOS/MS-DOS
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207-1941
227-2941
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rid, David N.

NOVEL GENES AND PROTEINS FOR TREATING
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US-09-256-703-2

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US-09-174-077-4
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Best Local Similarity
7; Conserve
                                                                           GENERAL INFORMATION:
                                                                                         Sequence 4, Application US/09174077 Patent No. 6329422
                                                                                                                                                                                                                                                   Best Local Similarity Matches 7; Conserv
                                                                                                                                                                                                                                                                                Query Match
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Patent No. 5972995
             APPLICANT: Fischer, Horst
APPLICANT: 11lek, Beate
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CYSTIC FIBROSIS THERAPY
FILE REFERENCE: 200116,403C1
 CURRENT APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (206) 682-60 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1479 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CYSTIC TITLE OF INVENTION: FIBROSIS THERAPY
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REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 16-OCT-1997
                                                                                                                                                                                      49 LSEKLER 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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Illek, Beate
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NUMBER:
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100.0%; Pred. No. 1.2e+02;
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US/09/174,077
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Pred. No.
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o. 1.2e+02;
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; SOFTWARE: PatentIn Ver. 2.0
; SEO ID NO 4
; LENGTH: 1479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-174-077-4
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Best Local Similarity
Trinas 7; Conserve
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US-07-637-621-2
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Best Local Similarity
Matches 7; Conserv
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EARLIER APPLICATION NUMBER: US 08/951,912
EARLIER FILING DATE: 1997-10-16
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                              TOPOLOGY: line MOLECULE TYPE: | ORIGINAL SOURCE:
                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1480 amino acids
                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: kagan, sarah a
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: antonarakis, stylianos e
APPLICANT: kazazian jr., haig h
TITLE OF INVENTION: CYSTIC FIBROSIS MUTATION CLUSTER
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
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                          155 LSEKLER 161
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polonia
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STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
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49 LSEKLER 55
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100.0%; Pred. No.
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                                                           Mismatches
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US-08-136-742A-2

Sequence 2, Application US/08136742A Patent No. 5670488

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Query Match
Best Local Similarity
Thes 7; Conserve
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,742A
FILING DATE: 02-DEC-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,478
FILING DATE: 02-DEC-1992
CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION: 514
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APPLICANT: Gregory, R.J., Armentano, D., Couture, L.A., Smith,
APPLICANT: A.E.
                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
                                                       TITLE OF INVENTION: DEOXYRIBONUCLEIC ACIDS CONTAINING
TITLE OF INVENTION: INACTIVATED HORMONE RESPONSIVE ELEMENTS
NUMBER OF SEQUENCES:
9
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:

NAME: Seide, Rochelle K.

REGISTRATION NUMBER: 32,300

REFERENCE/DOCKET NUMBER: A30668 (Genzyme Dkt. IG4-9.11)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 408-2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1480 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: GENE THERAPY FOR CYSTIC FIBROSIS NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                          APPLICANT: CHENG,
                                                                                                                                                                                                                                                                                                                                                                                                                                               155 LSEKLER 161
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ZIP: 10112
COUNTRY:
                                         CITY: FRAMINGHAM
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                    MASSACHUSETTS
                                                                                                                                                                          CHENG, SENG H.
DITULLIO, PAUL
EBERT, KARL M.
MEADE, HARRY M.
SMITH, ALAN E.
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100.0%; Pr
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Search completed: September 18, 2002, 16:37:34 Job time: 284 sec
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-135-809A-2
                                                                                                                                                Query Match
Best Local Similarity 100.
Thes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (508) 872-8400
TELEPAX: (508) 872-5415
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1480 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: IG-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIF: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                       155 LSEKLER 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/135,809A FILING DATE: 13-OCT-1993 CLASSIFICATION: 800
                                                                                                49 LSEKLER 55
                                                                                                                                                                            100.0%; P
                                                                                                                                                                          4.3%; Score 7; DB 1; Length 1480; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
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Search time (sec): 1625.180000
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Query: US-09-676-718A-1
Query length: 162
Database: EST:*
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gb_est2:BM476636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Results were produced by Copyright (c) 1993-2000
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COMMENT
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Percent Similarity:
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MetAlaAlaGlyProSerGlyCysLeuValProAlaPheGlyLysArgLe
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI0718 row: a column: 18
High quality sequence stop: 587.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1260 row: e column: 12
High quality sequence stop: 634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; V
Mammalla; Eutheria; Primates; Catarrhini;
1 (bases 1 to 642)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
BG399386
BG399386.1 GI:13292834
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
/Clone="IMAGE:455915"
/Clone_lib="NIH_MCC_75"
/Clone_lib="NIH_MCC_75"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: kidney; Vite_2: SiII (ggccattatggcc); S' and
SiII (ggccgcctcggcc); Site_2: SiII (ggccattatggcc); S' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
S'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                  VERSION
KEYWORDS
                                                                                                                                                                                                    seq_documentation_block:
LOCUS BG779736
        REFERENCE
                                                                                                                                          ACCESSION
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ORGANISM

Homo sapiens

EST

ıuman

mRNA sequence. BG779736

602668566F1 NIH_MGC_60

Homo

sapiens þ

clone linear

IMAGE: 4808032

υ

EST

mRNA CDNA

BG779736.1 GI:14050053

Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 664)

Chordata; Primates;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

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alignment_block:
US-09-676-718A-1 x
seq_name:
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Percent Similarity:
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                                                                              nIleLysTyrValArgG1ySerAspProValLeuLysLeuLeuAspAspA 134
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                         GTAGAAGTTCCTGAGTGAAAAGTTGGAACGCATA
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                                                     ValGluGluPheLeuSerGluLysLeuGluArgIle 162
                                                                                                                                     AATCAAGTATGTCCGTGGTTCAGACCCTGTATTAAAGCTTTTGGACGACA
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gb_est2:BG779736
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BASE COUNT
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TITLE
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101 ValGlnAlaPheValArgSerAspLysProLysLeuPheArgGlyLeuGl 117
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                                                                       84 laGlyAlaIleLeuGluValCysGly***LysLeuGlyArgPheProGln 100
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                                               CAGGAGCTATTCTTGAAGTTTGTGGATGAAAATTGGGAAGGTTCCCTCAA 325
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://image.llnl.gov
Plate: LLCM1660 row: d column: 17
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab_host="DHIUB (TI phage-resistant)"
/note="organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA.
5: and 3: adaptors were used in cloning as follows: 5:
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCACTG-T(3)BN-3'
sequence: 5'-ATTCTAGAGGCCGAGGCGGCCACTG-T(3)BN-3'
AUGTAGE
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(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
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118 c 170 g 197 t
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/clone_lib="NIH_MGC_60"
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/db_xref="taxon:9606"
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REFERENCE
AUTHORS
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ORGANISM
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ACCESSION
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                                                                                                                                                                                US-09-676-718A-1 x AV757896
                                                                                                                                                                                                                                    Percent Similarity:
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JOURNAL
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155
                                                                     105 ATGCCGCCTGGCCCACTGGCTGTCTGGTGCCGGCGTTTGGGCTACGGTT 154
                              17 uLeuLeuAlaThrValLeuGlnAlaValSerAlaPheGlyAlaGluPheS 34
                                                                                      1 MetAlaAlaGlyProSerGlyCysLeuValProAlaPheGlyLysArgLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens cDNA BM clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AV757896 BM Homo sapiens cDNA clone BMFALD04 5', mRNA sequence.
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Gu,Y., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zer,
Li, Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G.,
Yang,Y., Gao,G., Wang,Z., Zhang,Q., Chen,S., Han,Z. and Chen,Z.
                                                                                                                                                                                                                                                                         Quality:
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Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
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1 (bases 1 to 694)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: hanzg@chgc.sh.cn
This clone is available at CHGC
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98.765
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Gaps:
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REFERENCE
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BASE COUNT
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                                                                                                                                                                                                                 Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, 1201203, P. R. China Tel: 86-21-50801919 (ex.45)
                                                                                                                                                                                                                                                                                                                         l (bases I to /vv)
Xiao,H., Peng,Y., Song,H., Gu,Y., Yang,Y., Gao,G., Xu,X., Li,N.,
Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu
,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Chen,Z. and Han
                                                                                                                                                                         Email: hanzg@chgc.sh.cn
This clone is available at CHGC
                                                                                                                                                                                                                                                                                Unpublished (2000)
Contact: Zeguang H
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 700)
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                                                                                                                                                                                                                                                                                Zeguang Han
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130 c 171 g 204 t
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/db_xref="taxon:9606"
                                                                                                                                                             ocation/Qualifiers
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                          Site_2:
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REFERENCE
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US-09-676-718A-1 x
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Ratio:
                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 726)
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                mRNA sequence.
BI518529
                                                                                                                                                                                      EST
                                                                                                                                                                                                                                          603061650F1 NIH_MGC_118
                                                                                                                                                           Homo sapiens
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Primates;
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                                                                                      Gene
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    (LLNL)
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BASE COUNT
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http://image.llnl.gov
Plate: LLAMI1529 row: c column:
Plate: LLAMI1529 row: 724.
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Clone distribution: MGC clone distribution information can be
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this is a NIH_MGC Library."
1 134 c 172 g 224 t
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US-09-676-718A-1 x BI545979
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                                                 uLeuLeuAlaThrValLeuGlnAlaValSerAlaPheGlyAlaGluPheS
erSerGluAlaCysArgGluLeuGlyPheSerSerAsnLeuLeuCysSer
                                GTTGTTGGCGACTGTGCTTCAAGCGGTGTCTGCTTTTGGGGGCAGAGTTTT 118
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Email: cgapbs r@mail.nih.gov

Tissue procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11654 row: c column: 01
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Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
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1 (bases 1 to 739)
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
plate: LLCM1467 row: k column: 12
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/note="Organ: testis; Vector: pDNR-LIB (Clontech)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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KEYWORDS

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LOCUS BG613877
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Ratio:
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Homo sapiens
                                                                       mRNA sequence.
BG613877
                                                       BG613877.1
                     human.
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Gaps: 0
Percent Identity: 98.765
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IMAGE:4770860 5',
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alignment_block:
US-09-676-718A-1 x BG613877
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SArgGlyCysCysGlnGluGluAlaGlnPheGluThrLysLysLeuTyrA 84
                                                                                                                                                                               SerCysAspLeuLeuGlyGlnPheAsnLeuLeuGlnLeuAspProAspCy
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                                                                                                                                                          TCTTGTGATCTTCTCGGACAGTTCAACCTGCTTCAGCTGGATCCTGATTG
                                                                                                                                                                                                                                         CATCGGAGGCATGCAGAGAGTTAGGCTTTTCTAGCAACTTGCTTTGCAGC 176
                                                                             CAGAGGATGCTGTCAGGAGGAAGCACAATTTGAAACCAAAAAGCTGTATG
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plate: LLCM1638 row: g column: 21
High quality sequence stop: 714.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="embryonal carcinoma"
/lab host="PH108 (TI phage-resistant)"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc);
Souble-stranded cDNA was prepared from cell line RNA. 5/
and 3/ adaptors were used in cloning as follows: 5/
adaptor sequence: 5'-CACGGCCATATGTGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGCGGCGCGAATG-dT(30)BN-3'
(where B = A, C, Or G and N = A, C, G, Or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
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/clone_lib="NIH_MGC_61"
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/db_xref="taxon:9606"
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LOCUS BG777365
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plate: LLCM1651 row: k column:
High quality sequence stop: 731.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 746)
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                      203
                                                                                    /tissue_type="adenocarcinoma"
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/note="organ: prostate; Sit (ggccattatggcc);
/note="organ: prostate; Sit (ggccattatgcc);
/note="organ: planetate; Sit (ggccattatgcc);
/note="orga
                                                                     Library."
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/clone_lib="NIH_MGC_60"
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alignment_scores:

Quality:

Ratio:

819.00 5.119 98.765

Percent Identity: 98.765

162

Percent Similarity:

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REFERENCE
AUTHORS
TITLE
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ORGANISM
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LOCUS BI597212
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US-09-676-718A-1 x BG777365
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                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), S
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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BI597212
BI597212.1 GI:15490151
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Plate: LLAM11766 row
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          ValGluGluPheLeuSerGluLysLeuGluArgIle 162
                                         laGlyAlaIleLeuGluValCysGly***LysLeuGlyArgPheProGln
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                                                                                                                              156 TCTTGTGATCTTCTCGGACAGTTCAACCTGCTTCAGCTGGATCCTGATTG
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Contact: Genoscope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: segref@genoscope.cns.fr,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the NotI and Eco RV sites of the pcMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://fulllength.invitrogen.com"
140 c 185 g 246 t
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/sex="male"
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/clone="CS0DN004YB08"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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1 (bases 1 to 797)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    602549479F1 NIH_MGC_61 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                           218
            Library."
a 141 c
                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="IMAGE:4657338"
                                                                                                                                                                                                                                                                               ∕organism="Homo sapiens"
            192 g
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IMAGE:4657338 5',
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alignment_scores:

Quality:

819.00

Length:

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KEYWORDS
SOURCE
                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
LOCUS BG533149
                                                                                                                                                                                                                                                                                                                                                            seq_name:
                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                        VERSION
                                                                                                                                                                                                                                                                     ACCESSION
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Percent Similarity:
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                                                                                                                                    AUTHORS
TITLE
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                                                                                                                      JOURNAL
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                                                                                                                                                                                                                                                                                                                                                            gb_est2:BG533149
                                                                                                                                                                                                                                                                   mRNA sequence.
BG533149
                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 802)
                                                                                                                                                                                                                                                                                           BUZ bp mRNA linear EST 03-APR-2001 602580673F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4718490 5',
                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                       BG533149.1 GI:13524689
found through the
          CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
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Percent Identity: 98.765
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alignment_scores:
Quality:
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ValGlnAlaPheValArgSerAspLysProLysLeuPheArgGlyLeuGl
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Plate: LLCM1570 row:
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/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcggcttggcc); Site_2: SfiI (ggcattatggcc);
SfiI (ggcggcttggcc); Site_2: SfiI (ggcattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ACTGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ACTGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ACTGCAGGCCGATGATGC-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
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Gaps: 0
Percent Identity: 98.765
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alignment_scores:
Quality:
Ratio:
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AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                          alignment_block:
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VERSION
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LOCUS BG529329
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                                                                                                                                                                                                            Align seg 1/1 to: BG529329
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                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
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                                                                                                   66 GTTGTTGGCGACTGTGCTTCAAGCGGTGTCTGCTTTTTGGGGCAGAGTTTT
                                               17 uLeuLeuAlaThrValLeuGlnAlaValSerAlaPheGlyAlaGluPheS 34
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 808)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1499 row: b column: 12

High quality sequence stop: 732.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage=resistant)"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc);
Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ACKGCCCATTANGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGCATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Tebraticate (Table All Carlos Colonies)
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5.119
98.765
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Library."
1 145 c 200 g 241 t
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/db_xref="taxon:9606"
/clone="IMAGE:4687019"
/clone_lib="NIH_MGC_61"
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Gaps: 0
Percent Identity: 98.765
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466	151	416	134	366	117	316	101	266	84	216	67	166	51	116	34
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Sequence
Seq
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Database sequences: 383533
Database length: 122816752
Search time (sec): 43.970000
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Query: US-09-676-718A-1
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-Q-/cgn2_1/USPTO_spool/US98676718/runat_17092002_143433_21323/app_query.fasta_1.222
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        ValGlnAlaPheValArgSerAsp.LysProLysLeuPhe...
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APPLICANT: ENDECE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCUNA-260XX
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER APPLICATION NUMBER: 60/098,639
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FRSSTSEQ for Windows Version 3.0
SEQ ID NO 439
LENGTH: 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (1)...(578)
; OTHER INFORMATION: n =
US-09-385-982-439
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-568-459A-11+
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-487-826B-11+
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-213-448-2+
                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-09-385-982-439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 439, Application US/09385982
Patent No. 6262334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _documentation_block:
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                                                                                                                                                                   SerCysAspLeuLeuGlyGlnPheAsnLeuLeuGlnLeuAspProAspCy
                                                                         CAGAGGATGCTGTCAGGAGGAAGCACAATTTGAAACCAAAAAGCTGTATG
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; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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                                              504075 AGGCGCTGAACACCAACTGGGTCAAGCTCGAGGTGATTGCCGACGAACGC 504124
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APPLICANT: FRASER, CLAİRE M.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT FILING DAYE: 1998-06-24
CURRENT FILING DAYE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: FLEISCHMAN, ROBERT D. APPLICANT: WHITE, Owen R. APPLICANT: FRASER, Claire M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
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ORGANISM: Mycobacterium tuberculosis
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GlyArgPheProGlnValGlnAlaPheValArgSerAspLysProLysLe 112
                                                                                             lyAlaIle..........LeuGluValCysGly***LysLeu 95
                                                                                                                                         GGGGTGCCGCAGCGCCGCGGAAGCGGTCCTGACAGCGCAGTTGGCCCCGTG 504074
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Ratio:
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alignment_block:
                                                                                                                                                       alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-972-927-1
                                    US-09-676-718A-1 x US-08-972-927-1/rev
Align seg 1/1
                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08972927 Patent No. 6166290
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                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/061,328
FILING DATE: 08-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: DOY1e Leary Ph.D., Kathryn
REGISTRATION NUMBER: 35,317
REFERENCE/DOCKET NUMBER: 9596-1202
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1284
                                                                                                                                                                                                                                                                                                                                                   TELEX: 831-494
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 18-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 ..LysLeuLeuAspAspAsnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 uPheArgGlyLeuGlnIleLysTyrValArgGlySerAspProValLeu. 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: GLUTATHIONE-S-CONJUGATE TRANSPORT TITLE OF INVENTION: PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 215 - TELEPHONE: 215-567-2991
                                                                                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 18-NO
                                                                                                                                                                                                                                                                                                            LENGTH: 5232 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Philadelphia
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                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                   Ratio:
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  to reverse of: US-08-972-927-1
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Li, Ze-Sheng
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                                                                                                                                                                                                                                                      Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDMBER: US 60/061,328
08-OCT-1997
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                                                                                            77.50
1.615
56.471
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                                                                                            Gaps:
Percent Identity:
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  from:
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32 GluPheSerSerGluAlaCysArgGluLeuGlyPheSerSerAsnLeuLe

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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-912-227-1
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US-08-912-227-1
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                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/912,227
FILING DATE: Herewith
CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,058
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4170 TTGTG 4166
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                                                         MOLECULE TYPE: FEATURE:
                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Human Endokine Alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 CysGlnGluGluAlaGlnPheGluThrLysLysLeuTyrAlaGlyAlaIl 87
               NAME/KEY:
                                                                                                                                                                                                                                                                                            NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36.
REFERENCE/DOCKET NUMBER:
                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                               TELEPHONE:
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                                                                                                                                                             ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WASHINGTON
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                                                                                                                                                           1849 base pairs
                                                                                                                                                                                                                                202-371-2540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0,
                                                                                                 linear
                                                                                                                       double
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seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-972-927-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Rea, Ph
APPLICANT: Lu, Yu-
APPLICANT: L1, Ze-
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                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/972,927
FILING DATE: 18-NOV-1997
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                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,040
FILING DATE: 18-NOV-1996
PRIOR APPLICATION NUMBER: US 60/061,328
FILING DATE: 08-OCT-1997
                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
ATTORNEY/AGENT INFORMATION: NAME: Doyle Leary Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 laPheGlyAlaGluPheSerSerGluAlaCysArgGluLeuGlyPheSer 44
                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 19103-7086
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Philadelphia
STATE: Pennsylvani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C. STREET: One Commerce Square, 2005 Market Street, 22nd STREET: Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pennsylvania
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Lu, Yu-Ping
Li, Ze-Sheng
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1.562
48.980
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Kathryn
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seq_documentation_block:
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US-09-676-718A-1 x US-08-972-927-4/rev
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08441139 Patent No. 5773245
                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 5175 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4141 TTGTG 4137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4385 GAATTCTTCTCGGATGGTCTTTTGGATGAGAACATCAGTTCTTACGTCAA 4336
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1284
                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wittrup, Dr. Karl D. APPLICANT: Robinson, Anne S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 heVal 105
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                                                                                                                                                                               STREET: 400 Garde CITY: Garden City
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STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 215 July 1 TELEPHONE: 215-567-2991
                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 215-5
                                                                                                                      ZIP: 11530
                                                                                                                                                               STATE:
                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-441-139-6
                                                                                                                                                    NY.
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                                                                                                                                                                                                      400 Garden City Plaza
                                                                                                                                        USA
                                                                                                                                                                                                                          SCULLY, SCOTT, MURPHY & PRESSER
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1.585
55.294
                                                                                                                                                                                                                                                                                          METHODS FOR INCREASING SECRETION OF RECOMBINANTLY EXPRESSED PROTEINS
                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9596-1202
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seq_documentation_block:
; Sequence 42, Application US/08178477B
; Patent No. 5756343
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US-09-676-718A-1 x US-08-441-139-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-178-477B-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-441-139-6
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Patent No. 3/JULE
GENERAL INFORMATION:
GENERAL INFORMATION: CLOS, JOACHIM;
APPLICANT: WESTWOOD, J. TIMOTHY.; RABINDRAN,
APPLICANT: WESTWOOD, J. TIMOTHY.; RABINDRAN,
TITLE OF INVENTION: CELL STRESS
TITLE OF INVENTION: TRANSCRIPTIONAL FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1931 TGTTCCCCAAATTGAAGTCACGTTTGAAGTCGAT.......GCCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1881 AACCTTCTTGGAAAATTTGACCTTCGTGGTATTCCTCCTGCCCCTCGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2092 AAGAATTCGCTGAAGAAGATAAGATTTTGAAG 2123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1972 GTGTTTTGACTGTTTCAGCCGTCGACAAGTCTGGTAAGGGTAAGCCTGAG 2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 lyAsnIleAlaGluGluLeuSerIleLeuLys 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US OF FILING DATE: 06-JUL-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-MAY-15-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 laIleLeuGluValCysGly...***LysLeuGlyArgPheProGlnVal 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 AspLeuLeuGlyGlnPheAsnLeuLeuGlnLeuAspProAspCysArgGl
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2574 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: DiGiglio, Frank REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlnAlaPheValArgSerAspLysProLysLeuPheArgGlyLeuGlnIl 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....TCTGAGGAAGATATCGAGCGCATGGTTAAGGAGGCCG 209:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eLysTyrValArgGlySerAspProValLeuLysLeuLeuAspAspAsnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YCYSCYSGlnGluGluAlaGlnPheGluThrLysLysLeuTyrAlaGlyA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
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15-MAY-1995
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1.396
56.383
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Percent Identity: 27.660
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN

COUNTRY:

USA

NEW YORK

345 PARK AVENUE

NEW YORK

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alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-178-477B-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: US-08-178-477B-42 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 421792
INFORMATION FOR SEQ ID NO:
                                             1681
                                                                                                                                                                                                                                                                                                                                                                                                                                          1919
                                                                                                                                                                                                    1781
                                                                                                                    1731 GGCTGCCTCTTCCACGCCGTCGGGAAGCAGAGCGTCTTCAAAAATATCCG 1682
                                                                                                                                                                                                                                                                              1825 CCAGCAGCGTACTGTTGGTGGGCACATCGAAGTTGCTGGCA.....AAC 1782
                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
      105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/617,910
FILING DATE: 26-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY |
                                                                                 90
                                                                                                                                                             75
                                                                                                                                                                                                                                                                                                                       43
                                                                                                                                                                                                                                           60
                                                                                                                                                                                                                                                                                                                                                                                               28 ....AlaPheGlyAlaGluPheSerSerGluAlaCysArgGluLeuGlyP 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 PheGlyLysArgLeuLeuAlaThrValLeuGlnAlaValSer.... 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 07-JAN CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 37, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
                                                                                                                                                                                                                                   LeuLeuGlnLeuAspProAspCysArgGly...CysCysGlnGluGlu.. 74
                                                                                                                                                                                                                                                                                                                   heSerSerAsnLeuLeuCysSerSerCysAspLeuLeuGlyGlnPheAsn 59
                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCTCAGCGCCACTGTATTTGGCCACAGCCATGCCCTCTTCCTCAGATGC 1870
...ValArgSerAspLysProLysLeuPheArgGly......
                                        TCGGCATATCCTCACTGATGAAGTTGACACTGTACAGATCGTTCGCGGGA 1632
                                                                             alCysGly***LysLeuGlyArgPheProGlnValGlnAlaPhe..... 104
                                                                                                                                                                                                  TTGCCGCTGCTCACTGTCGATTGCCCCAAATTTTTGCTGCTGGTCCAGTTT 1732
                                                                                                                                                         ....AlaGlnPheGluThrLysLysLeuTyrAlaGlyAlaIleLeuGluV 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
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CAROL M. GRUPPI
37,341
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(212) 751-6849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.50
0.827
50.299
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alignment_block:
US-09-676-718A-1 x US-08-441-139-1
                                                                                         alignment_scores:
Quality:
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; LOCATION:
US-08-441-139-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1581 CATTGGCTGGACCATCACATCAGGTTGCGTACTATGCTGGATGC..... 1538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: DIG19110, Frank S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Relaction DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 ValLeuLysLeuLeuAspAspAsnGlyAsnIleAlaGluGluLeuSerIl 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 eLeuLysTrpAsnThrAspSerValGluGluPheLeuSerGluLysLeu 159
                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wittrup, Dr. Karl D. APPLICANT: Robinson, Anne S. TITLE OF INVENTION: RECOMBINANT
                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Garden City
STATE: NY
                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/441,139 FILING DATE: 15-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                                                                                             ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-441-139-1
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                                                                                                                                                                                                                                                                                          nucleic acid
                                                                       Ratio:
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                                                                                                                                                                                                                                                                                                           2780 base pairs
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285..2333
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                                                        69.00
1.015
47.552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METHODS FOR INCREASING SECRETION RECOMBINANTLY EXPRESSED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                         Percent
                                                        Gaps:
: Identity:
                                                                                           Length:
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alignment_scores:
Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                           ; TYPE: DNA
GRGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
; Sequence 1, Application US/09103840A
; Patent No. 6294328
alignment_block:
US-09-676-718A-1 x US-09-103-840A-1
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                                                                                                                                                                                                                                                                                                                 APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007.00
CUGRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2114 AACCTTATTAGATGCTGCTAACGATGTTTAGAATGGTTAGATGATAACT 2163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2064 AACCAAGTTAATGGTGACCTAGGTGAAAAATTGGAAGAAGAAGACAAGGA 2113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2014 CCAAGGTTGAATCTAGAAACAAATTAGAAAACTACGCTCACTCTTTGAAA 2063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1914 ATCACCATCACTAACGATAAAGGTAGATTAACCCAAGAAGAGAGTTGATAG 1963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1864 GTATTCTGAAGGTGTCTGCCACAGATAAGGGAACTGGTAAATCCGAATCT 1913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1823 TGTACCTCAAATTGAAGTCACATTT......GCACTTGACGCTAATG 1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1773 AATCTATTAGGTAAGTTTGAATTAACCGGCATTCCACCAGCACCAAGAGG 1822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alGluGluPheLeuSerGluLysLeuGlu 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....SerIleLeuLysTrpAsnThrAspSerV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATGGTTGAAGAGGCTGAAAAATTCGCTTCTGAAGACGCTTCTATCAAGG 2013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yCysCysGlnGluGluAlaGlnPheGluThrLysLysLeuTyrAlaGlyA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.00
0.883
54.610
                                                                        Gaps:
Percent Identity:
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Align seg 1/1 to: US-09-103-840A-1 from: 1 to: 4411529

5024 5024 5025 5026 5026 5026 5026 5027 5027
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alignment_block:
US-09-676-718A-1 x US-08-752-760A-1/rev
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                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Topfer, Reinha
APPLICANT: Hausmann, Ludg
APPLICANT: Schell, Jozef
TITLE OF INVENTION: GLYCE
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: US-08-752-760A-1 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08605150A Patent No. 6103520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3750 GGCCAGCAGTTCTCCTCG...GCGATGATGGAACTGGGCACAGAGGGGCT 3704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3703 ACTGCTGCTGCGCATGTAGCTCGAGGCCAGTCTCGTCGCTGTCATGG 3654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3653 CGGCTGCGGCTG...CCGCGGCGCTGCGGCGTGCTCAAGCGACGAGTTC 3607
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,150
FILING DATE: 01-MAR-1996
CLASSIFICATION: 800
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Klein & Szekeres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 35081 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 **LysLeuGlyArgPheProGlnValGlnAlaPheValArgSerAspLys 109 *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 nLeuLeu.CysSerSerCysAspLeuLeuGlyGlnPheAsnLeu..... 60 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 GlyAlaGluPheSerSerGluAlaCysArgGluLeuGlyPheSerSerAs 46
                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ...LeuGlnLeuAspProAspCysArgGlyCysCysGlnGluGluAlaGl 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCATCCTGGCAGGCGGGTTGTCAAATAAG 3486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCACGGTCGCGTAGGTCATGGTCGAGGAATTTGCTGGAAGCACTGGGC. 3558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                              92715
                                                                                                                                                                                                                                                         Irvine
                                                                                                                                                                                                                                       CA
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                                                                                                                                                                                                                                                                                4199 Campus Drive, Suite 700
                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Topfer, Reinhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212-705-5020
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1.241
57.447
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Ludger
                                        US/08/605,150A
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                                                                                   Version
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5
31.915
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alignment_block:
US-09-676-718A-1 x US-08-605-150A-3/rev
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    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: US-08-605-150A-3 from: 1
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727
                                                                                                                                                                                                                                     874 TTAACAGATGGAAACAAAAGCTTGGAGAACGCTTTCATCTCCCCGCAGCCC 825
                                                                                                                                                                                                                                                                                                                                                                                                    974 GCCATTCTTTGCAAAAGCCTCAGCGACTTTTCTGTTTCTTCCGCCCAAAC 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT\EP94\0293
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4329827.3
                                                                             774 CAAAACCCGCTGCTATGGCCACAATATTCTTCAG...TGTTCCACAAAGC 728
                                                                                                                                                        824 GATCCTCATAATTGCCGCTTTTGTGTTGTTTCCCCATCTCCAATCCATCAA 775
                                                                                                                                                                                                                                                                                                                     924 AAGTTGTGATGAGATCAGCGACTCCGCAGCTCTCGAAAAAAGTAGTGTCC 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Cupl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 28,675
REFERENCE/DOCKET NUMBER: 54
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 03-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
LIBRARY: ZAP cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                     95
                                                                                                                                                                                                  64
                                                                                                                79 rLys...LysLeuTyrAlaGlyAlaIleLeuGluValCysGly***LysL 95
                                                                                                                                                                                                                                                                                                                                                          36 uAlaCysArgGluLeuGlyPheSerSerAsnLeuLeuCysSerSerCys. 52
                                                                                                                                                                                                                                                                                                                                                                                                                                         20 AlaThrValLeuGlnAlaValSerAlaPheGlyAlaGluPheSerSerGl 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONE: C1GPDH109
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                                                                                                                                                                                 AspPro...AspCysArgGlyCysCysGlnGluGluAlaGlnPheGluTh 79
                                   euGlyArgPhe 98
TCTACTCCTTC 717
                                                                                                                                                                                                                                                                           Szekeres, Gabor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
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45..1187
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seq_documentation_block:
 Sequence 1, Application US/08942686
 Patent No. 6183988
 GENERAL INFORMATION:

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-942-686-1

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alignment_block:
US-09-676-718A-1 x US-08-942-686-1
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; LOCATION:
US-08-942-686-1
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Ratio:
Percent Similarity:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2905 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-08-942-686-1 from: 1 to: 2905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,347

FILING DATE: 02-0CT-1996

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.4330001/JAG/BJD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                         2035 TGAGGAACAGTTGAAATGTGAGTTCCTCCTCTTGAAAGTC..... 2074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,686
FILING DATE: 02-OCT-1997
                                                                    2117 TATTATTATATAGAGAGGCGTGTCAAGGCCTGAAGGAGCCCATGTGGTT 2166
                                                                                                                                                      2075 .... TATTGCTGT...TCTGAGAGCTCCTTTTTTGCCAAGATTCCATAC 2116
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TITLE OF INVENTION: LEUKCCYTE-SPECIFIC PROTEIN AND GENE, AND TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                              67 ysArgGlyCysCysGlnGluGluAlaGlnPheGluThrLysLysLeuTyr 83
                                                                                                                                                                                                                                                                                                                                                               34 SerSerGluAlaCysArgGluLeuGlyPheSerSerAsnLeuLeuCysSe 50
                      95 uGlyArg.....
                                                                                                       84 AlaGlyAlaIleLeuGluValCys...Gly***Lys......Le 95
                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: STERNE, KESSLER, GOLDSTEIN AND FOX, P.L.L.C. STREET: 1100 NEW YORK AVENUE, N.W. SUITE 600
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Bloch, Kenneth D
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107..2365
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1.023
48.872
.....PheProGlnValGlnA 103
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63LeuAspProAspCysArgG 69 13LeuAspProAspCysArgG 69 2554 CAACCACATGCACAATGCTCTTTCACTTTCATTTCATTT	
58 PheasnleuleuGln	
44SerSerAsnLeuLeuCysSerSerCysAspLeuLeuGlyGln 57 ::: :::: ::: 2754 TTCGGAGATCAGGAAACATGATTTCAGCCCCTGATGATCTTATAGGTCCA 2705	
27 ralapheGlyAlaGluPheSerSerGluAlaCysArgGluLeuGlyPhe. 43 : ::: ::::::	
14 GlyLysArgLeuLeuLeuAlaThrValLeuGlnAlaValSe 27	
Align seg 1/1 to reverse of: US-09-180-439-1 from: 1 to: 3979	
alignment_block: US-09-676-718A-1 x US-09-180-439-1/rev	
alignment_scores: Quality: 66.00 Length: 179 Ratio: 0.857 Gaps: 7 Percent Similarity: 43.017 Percent Identity: 21.788	
TACAAGTACAAGGATTTTGGCCAAATGGGATTTAGACTGGAGGTGAGTTTTTGGCTAAATGGGATTTAGACTGGAGGTTAGACTGGAGTTTTTTGAGAGTAGAGTTTTAGACTGGAGTTTTTTTT	
ICATIONAL AND ASSEMBLE STREET STREE	
CCCAAGTGGAGG	

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alignment_block:
US-09-676-718A-1 x US-09-180-439-2/rev
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CURRENT APPLICATION NUMBER: US/09/180,439
CURRENT FILING DATE: 1998-12-06
EARLIER APPLICATION NUMBER: PCT/GB97/01249
EARLIER APPLICATION NUMBER: GB 9609681.3
EARLIER APPLICATION NUMBER: GB 961924.5
EARLIER FILING DATE: 1996-05-09
EARLIER FILING DATE: 1996-09-24
NUMBER OF SEO ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA ; ORGANISM: Lycopersicon esculentum US-09-180-439-2
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                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Dixon, mark S
APPLICANT: Hatzixanthis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09180439 Patent No. 6225532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jones, David A APPLICANT: Jones, Jonathan DG
                                                                                                                                                           2854 GGTTCCTCCATTGTTTTATCAACTGTCCTCATCCCTTTCAAATGTTCAAA 2805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2410 TTGTTTCTGCCAAAATCAAGTATTTTTAGTGATGTTAAATTGGAAATAGA 236:
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                                                                  2510 AAAATTTGTTGGAAGAGTCCCAGAAAGTTTGTTATTCTGCATATCAAAAA 2461
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                          44
                                                                                                      27 rAlaPheGlyAlaGluPheSerSerGluAlaCysArgGluLeuGlyPhe. 43
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SerSerAsnLeuLeuCysSerSerCysAspLeuLeuGlyGln 57
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Gaps:
Percent Identity:
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alignment_block: us-09-180-439-7/rev
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; Sequence 7, Application US/09180439
; Patent No. 6225532
                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                           ; ORGANISM: Lycopersicon esculentum US-09-180-439-7
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  Align seg 1/1 to reverse of: US-09-180-439-7
                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 7
LENGTH: 4123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hatzixanthis, Kostas
APPLICANT: Jones, David A
APPLICANT: Jones, Jonathan DG
TITLE OF INVENTION: Plant pathogen resistance
FILE REFERENCE: 620 - 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/180,439 CURRENT FILING DATE: 1998-12-06 EARLIER APPLICATION NUMBER: PCT/GB97/01249 EARLIER FILING DATE: 1997-05-08 EARLIER APPLICATION NUMBER: GB 9609681.3 EARLIER FILING DATE: 1996-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER FILING DATE: 1996-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: GB 9619924.5
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                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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Percent Identity:
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to: 4123
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14		27
998	GTTCCTCCATTGTTTTATCAACTGTCCTCATCCCTTTCAAATGTTCAAA	2949
27	rAlaPheGlyAlaGluPheSerSerGluAlaCysArgGluLeuGlyPhe. 4	ū
2948	TAGACTCGTTGGTAAGTCTTGCGAGAATGCATTGCGAGAGAGA	2899
44		57
868	TTCGGAGATCAGGAAACATGATTTCAGCCCCTGATGATCTTATAGGTCCA	2849
58	PheAsnLeuGln6	52
848	TGCAATTTATTCGATGTCAACCTTAAAACTCTCAGCTCTGGCAAAGTTCC	2799
63	LeuAspProAspCysArgG 6	9
2798	CAACCACATGGGAAATGTGTCGTTGAGTTGATTGTCTCCTAAATCAAGAA :	2749
69	lyCysCysGlnGluGluAlaGlnPheGluThrLysLysLeuTyrAlaGly 8	5
2748	CTTGCAGCTTTTTGCAATTGTCCAAAGACCGAGGGATTTCATCT	2705
86	AlaIleLeuGluValCysGly***LysLeu9	5
2704	GCT	2655
96		107
2654		2605
107		107
2604	CCTGGAGGCTACTAATATTGCCAAAAAATTGTGGTATTGCTCCCTCC	2555
108		121
2554	TTGTTTCTGCCAAAATCAAGTATTTTTAGTGATGTTAAATTGGAAATAGA	2505
121	121 lArgGlySerAspProValLeuLysLeuLeuAspAsp 133	
504	TO A COUNTY	

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Database: N_Geneseq_032802:*
Database sequences: 1736436
Database length: 858457221
Search time (sec): 201.290000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query length: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of: US-09-676-718A-1 to: N_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Results were Copyright (c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002 5:44
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Compugen
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ougen Ltd.
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Jen | Documentation | DAT:AAA4484 + 819.00 1991.55 |
DAT:AAA4484 + 819.00 1893.70 | 5.5 |
DAT:AAA34464 + 819.00 1893.70 | 5.5 |
DAT:AAA34660 + 819.00 1890.56 | 5.5 |
AT:AAA34660 + 819.00 1890.56 | 5.5 |
AT:AAA34468 + 751.00 1734.15 | 3.0 |
T:AAA343009 + 742.00 1719.76.16 | 9.8e |
T:AAA16434 + 552.50 1276.16 | 9.8e |
T:AAA343003 + 613.50 1418.66 | 1.1e |
T:AAA343004 + 274.00 | 603.84 | 2.8e |
AAA447500 + 286.50 | 507.92 | 6.1e |
T:AAA34325 + 226.50 | 507.92 | 6.1e |
T:AAA36995 + 172.50 | 385.18 | 4.2e |
AAA605398 + 172.50 | 385.18 | 4.2e |
T:AAA36995 + 172.50 | 385.18 | 4.2e |
T:AAA36995 + 172.50 | 385.18 | 4.2e |
T:AAA36995 + 132.50 | 301.49 | 1.9e |
T:AAA36995 + 132.50 | 301.49 | 1.9e |
T:AAA36989 + 132.50 | 301.49 | 1.9e |
T:AAA36998 + 132.50 | 301.49 | 1.9e |
T:AAA60598 + 122.50 | 301.49 | 1.9e |
T:AAA605998 + 122.50 | 301.49 | 1.9e |
T:AAA605998 + 122.50 | 301.49 | 1.9e |
T:AAA605998 + 122.50
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CC AAA43426 to AAA45925 represent specifically claimed secreted expressed sequence tags (sESTs), isolated from human, mouse, chicken and rat tissue sources. The sESTs can have a range of activities depending on the tissues they were isolated from. The activities include: chemotactic; proliferative; immunomodulatory; haematopoietic; chemotactic; analgesic; haematatic; thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; antivral; antidiabetic; antiasthmatic; vulnerary; antiulcer; osteopathic; neuroprotective; concorropic; antiparkinsonian; antipsoriatic; cerebroprotective; anticorvulsant; and anidepressant. The sESTs can be used for gene therapy and in vaccines. The sESTs are useful as probes for the identification and isolation of full-length cDNAs and genomic DNA concludes which correspond to the sESTs. Proteins encoded by the sESTs are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions (asthma), myeloid on lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoparthritis, central nervous system disorders

Claim 1; Page 474; 803pp; English.

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/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:AAS91142 + 
/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAS0995 + 
/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAS02330 + 
/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1994.DAT:AAQ55970 + 
/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAX91416 +
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ID AAA44484 standard:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expressed sequence tag; EST; probe; chemotactic; proliferative; immunomodulatory; haematopoletic; chemokinetic; analgesic; haemostatic thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian; antivire; osteopathic; neuroprotective; nootropic; antipsoriatic; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; butn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
                                                                                                                                                                                                                                                                                                             Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (SESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA4484 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted expressed sequence tag SEQ ID NO:1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mouse; chicken; rat;
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                                                                                                                                                                                                                                                                                                                                                                                                        Bowman
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33.4
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Homo

sapiens

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seq_documentation_block:
ID AAZ34464 standard; cE
XX
AC AAZ34464;
XX
DT 01-FEB-2000 (first e
XX
DE Human 15 kDa selenopr
XX
KW Selenoprotein; seleni
KW prostate cancer; diag
XX
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US-09-676-718A-1 x AAA44484
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Quality:
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                                                                                                                                                                                                                                                                                                        428
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                             Selenoprotein; selenium; differential expression; tumour; human;
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|||||||||||||||||||||
ATCAAGTATGTCCGTGGTTCAGACCCTGTATTAAAGCTTTTGGACGACA 427
                                                                                                                                                                                                                                                         ValGluGluPheLeuSerGluLysLeuGluArgIle
                                                                                                                                                                                                                                                                                                                       sArgGlyCysCysGlnGluGluAlaGlnPheGluThrLysLysLeuTyrA
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                                                                                                                                                                                                                                                                                                     GTCCAAGCTTTTGTTAGGAGTGATAAACCCAAACTGTTCAGAGGACTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laGlyAlaIleLeuGluValCysGly***LysLeuGlyArgPheProGln 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MetAlaAlaGlyProSerGlyCysLeuValProAlaPheGlyLysArgLe
                                                                                                                                                                                                         /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT: AAZ34464
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                  cancer; diagnosis; polymorphism; gene therapy; ss.
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Gaps: 0
Percent Identity: 98.765
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CC for recognition of this UGA as a codon for selenocysteries.

CC for recognition of this UGA as a codon for selenocysteries.

CC structure is termed a stem-loop selenocysteine insertion sequence

CC (SECIS) element. 2 Polymorphisms have been detected in the 3'UTR

CC of the human selenoprotein CDNA, one of them located within the

CC SECIS. There is a correlation between the presence of these

CC polymorphisms and the presence of cancer, including prostate cancer.

CC The polymorphisms are more prevalent in the African American

CC used as an indicator of the need for dietary selenium

CC supplementation to inhibit tumour development. Probes and primers

CC useful for detecting polymorphisms in the cDNA are disclosed. Also

CC provided are compositions and methods for determining the effect of

CC candidate tumour therapeutics on the expression of the 15 kDa

CC selenoprotein. Gene therapy can be used to treat tumors by

CC overexpressing the 15 kDa selenoprotein, or in the cells of

CC abnormally low amount of 15 kDa selenoprotein, or in the cells of

CC high-risk patients. The 15 kDa selenoprotein gene maps to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a human cDNA sequence encoding a 15 kDa selenoprotein (see AAY32112). The coding region (also claimed) includes an in-frame TGA codon encoding selenocysteine. conserved stem-loop structure (see also AAZ34473) in the 3' untranslated region (3'UTR) of the corresponding mRNA is essential for recognition of this UGA as a codon for selenocysteine. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated selenoprotein polypeptides, used to develop products for detecting susceptibility to or treating cancers e.g. prostate cancers
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281..283
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in Claim 13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
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Sequence 1244

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seq_documentation_block:
ID AAX00680 standard;
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US-09-676-718A-1 x AAZ34464
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                                                                     Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroid; tis; thyroid; digestion; osteoporosis; arthritis; testis; lung; thyroid; tis; thyroid; digestion;
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WO9842738-A1
                                                             endocrine;
                                                                                                                                                                                                               Human secreted protein gene 70 clone HMSGT42.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sArgGlyCysCysGlnGluGluAlaGlnPheGluThrLysLysLeuTyrA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MetAlaAlaGlyProSerGlyCysLeuValProAlaPheGlyLysArgLe
                                                                                                                                                                                                                                                                                                                                                                                                                      ValGluGluPheLeuSerGluLysLeuGluArgIle 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     snGlyAsnIleAlaGluGluLeuSerIleLeuLysTrpAsnThrAspSer 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATCAAGTATGTCCGTGGTTCAGACCCTGTATTAAAGCTTTTGGACGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValGlnAlaPheValArgSerAspLysProLysLeuPheArgGlyLeuGl 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGAGCTATTCTTGAAGTTTGTGGATGAAAATTGGGAAGGTTCCCTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGAGGATGCTGTCAGGAGGAAGCACAATTTGAAACCAAAAAGCTGTATG
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                                                                                                                                                                                                                                                                                                                                                                                                   GTAGAAGAATTCCTGAGTGAAAAGTTGGAACGCATA
                                                                                                                                                                                                                                                                                                                                                                /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:AAX00680
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Ratio:
                                                              metabolism;
                                                                                                                                                                                                                                                (first entry)
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5.119
98.765
                                                                                                                                                                                                                                                                                                                   DNA;
                                                              regulation; malabsorption; gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from:
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Identity: 98.765
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alignment_block: US-09-676-718A-1

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Percent Similarity:

Align seg 1/1

6

AAX00680

from:

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to: 1563

MetAlaAlaGlyProSerGlyCysLeuValProAlaPheGlyLysArgLe

17

alignment_scores:

Quality: Ratio:

819.00 5.119 98.765

Length: Gaps: Percent Identity:

162 0 98.765

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generate fusion proteins by linking to the gene can be used to generate fusion proteins by linking to the gene can be used to protein (e.g. AAX00602) for increasing the stability of the fused to protein as compared to the human protein only.

The invention relates to 87 novel genes and their fragments (nucleic acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the amount of the new polynucleotides. Specific uses are described for each of the 87 polynucleotides, based on which tissues they are most highly expressed in (see AAX00611 for described uses).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY 1997
21-MAR 1997
21-MAR 1997
21-MAR 1997
21-MAR 1997
21-MAR 1997
30-MAY 1997
                                                                                                                                                                                                  This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to
                                                                                                                                                                                                                                                         Claim 1; Page 230-231; 385pp; English.
                                                                                                                                                                                                                                                                                        disorders, immune diseases, inflammation
                                                                                                                                                                                                                                                                                                     New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological
Sequence 1563 BP; 478 A; 252 C; 301 G; 531 T; 1 other
                                                                                                                                                                                                                                                                                                                                               WPI; 1999-070066/06.
P-PSDB; AAW67876.
                                                                                                                                                                                                                                                                                                                                                                                                       Greene JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -MAY-1997
-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                         CA,
                                                                                                                                                                                                                                                                                                                                                                                         Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                               Duan R, Ebner DW, Movre un JS, Lafleur DW, Young P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            970S-0048094.
970S-0048095.
970S-0048099.
970S-0048099.
970S-0048135.
970S-0048154.
970S-0048186.
970S-0048187.
970S-0048187.
970S-0048350.
970S-0048351.
970S-0048351.
970S-0048353.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Ferrie AM,
                                                                                                                                                                                                                                                                                                                                                                                                        Moore
                                                                                                                                                                                                                                                                                                                                                                                                        PA,
                                                                                                                                                                                                                                                                                        or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                      Florence KA;
                                                                                                                                                                                                                                                                                                                                                                                                        Νi J,
                                                                                                                                                                                                                                                                                                                                                                                                        Olsen HS
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seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _documentation_block:
WPI;
                                                                                                                                                                                                                                                                              Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; prolliferative disorder; wound; infectious disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440
                                                                                                                                                                                                                                                 Homo sapiens.
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                                Rosen CA,
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                                                                                                                 12-MAR-1999;
                                                                 ROSE/) ROSEN
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 2000-587513/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:AAF16335
                                                                                  HUMAN
                                Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                               GENOME SCI INC
                                                                                                               99US-0124270.
                                                                                                                                                                                                                                                                                                                                                                                               cancer antigen nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1637
                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                 NO:770
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AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic
                                                                                       or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
                                                                disorders, wounds, and infectious diseases. AAF16506 to \lambda AAB57303 represent sequences used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prostate cancer associated gene sequences, referred to cancer antigens, useful for treatment, prevention, and
  Sequence 1637
                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 1189-1190; 2338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders such as prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB57132.
  вP;
500 A;
273 C;
323 G;
541 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         as prostate
diagnosis of
                                                                    of the
                                                                  present
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alignment_block: US-09-676-718A-1 x AAF16335 alignment_scores: Align seg 1/1 Ratio: Percent Similarity: 349 199 101 ValGlnAlaPheValArgSerAspLysProLysLeuPheArgGlýLeuGl 299 249 TCTTGTGATCTTCTCGGACAGTTCAACCTGCTTCAGCTGGATCCTGATTG 149 GTTGTTGGCGACTGTGCTTCAAGCGGTGTCTGCTTTTGGGGCAGAGTTTT 84 67 51 34 erSerGluAlaCysArgGluLeuGlyPheSerSerAsnLeuLeuCysSer 17 uLeuLeuAlaThrValLeuGlnAlaValSerAlaPheGlyAlaGluPheS 99 1 MetalaalaGlyProSerGlyCysLeuValProAlaPheGlyLysArgLe snGlyAsnIleAlaGluGluLeuSerIleLeuLysTrpAsnThrAspSer nIleLysTyrValArgGlySerAspProValLeuLysLeuLeuAspAspA laGlyAlaIleLeuGluValCysGly***LysLeuGlyArgPheProGln CAGAGGATGCTGTCAGGAGGAAGCACAATTTGAAACCAAAAAGCTGTATG sArgGlyCysCysGlnGluGluAlaGlnPheGluThrLysLysLeuTyrA SerCysAspLeuLeuGlyGlnPheAsnLeuLeuGlnLeuAspProAspCy AATCAAGTATGTCCGTGGTTCAGACCCTGTATTAAAGCTTTTGGACGACA GTCCAAGCTTTTGTTAGGAGTGATAAACCCAAACTGTTCAGAGGACTGCA CAGGAGCTATTCTTGAAGTTTGTGGATGAAAATTGGGAAGGTTCCCTCAA ATGGCGGCTGGGCCGAGTGGGTGTCTGGTGCCGGCGTTTGGGCTACGGTT Quality: AAF16335 819.00 5.119 98.765 from: 1 Percent Identity: . 6 162 0 98.765 498 134 448 100 198 150 398 298 67 248 50 34

ValGluGluPheLeuSerGluLysLeuGluArgIle

549

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alignment_scores:
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                                                                                                                  of the corresponding mRNA is essential for recognition of this UGA as a codon for selenocysteine. This structure is termed a stem-loop selenocysteine insertion sequence (SECIS) element. 2 C polymorphisms have been detected in the 3'UTR of the human selenoprotein cDNA (see AAZ34464). There is a correlation between the presence of these polymorphisms and the presence of cancer. The determination of an individual's genotype may be used as an indicator of the need for dietary selenium supplementation to inhibit tumour development. Gene therapy can be used to treat tumors by overexpressing the 15 kDa selenoprotein. The availability of the murine cDNA allows the production of rem therapentic and knock-out mice useful for assessment of new therapeutic agents.
 Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                       The present sequence represents a murine cDNA sequence encoding a 15 kba selenoprotein (see AAY32113). The coding region includes an in-frame TGA codon encoding selenocysteine. A conserved stem-loop structure (see also AA234474) in the 3' untranslated region (3'UTR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                           Sequence 1216 BP;
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 13; Page 58-59; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated selenoprotein polypeptides, used to develop products for detecting susceptibility to or treating cancers e.g. prostate cancers {\tt e.g.}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Selenoprotein; selenium; differential expression; tumour; mouse; prostate cancer; diagnosis; polymorphism; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse 15 kDa selenoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gladyshev VN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-013045/01.
DB; AAY32113.
                              Quality:
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95.679
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/note= "stem-loop selenocysteine insertion sequence
(SECIS element)"
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                                                                                        359 A; 242 C; 275 G; 340 T; 0 other;
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Gaps:
Percent Identity:
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seq_documentation_block:
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US-09-676-718A-1 x AAZ34468
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                                                                                                                                                                Human; 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability;
                                                                                                                                                                                                                                                                                                                                                                                                                             411
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         09-APR-1998;
28-APR-1998;
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                                                                                                                                                                                                                                                                                                       AAZ43009 standard;
                                                                                                                                                                                                                                                                                                                                                                        461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 CGTCAGAGGCATGCAGAGAGTTGGGTTTCTCCAGCAACTTGCTCTGCAGC
                                                 09-APR-1999;
                                                                            21-OCT-1999
                                                                                                     WO9953051-A2
                                                                                                                              Homo sapiens
                                                                                                                                                       regulation; identification; ss.
                                                                                                                                                                                                                        Human 5' EST isolated from a cDNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nIleLysTyrValArgGlySerAspProValLeuLysLeuLeuAspAspA 134
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                       98US-0057719
           9805-0069047
                                                 99WO-IB00712
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alignment_block:
US-09-676-718A-1 x AAZ43009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences, corresponding to human secreted proteins. AAY64651 to AAY65438 represent the EST-related proteins corresponding to AAZ422 AAZ43052. The 5' ESTs can be used for producing secreted human gene products. They can be used to identify and isolate 5' untranslated
  527
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                             101 ValGlnAlaPheValArgSerAspLysProLysLeuPheArgGlyLeuG1 117
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                                                                                                            CAGGAGCTATTCTTGAAGTTTGTGGATGAAAATTGGGAAGGTTCCCTCAA
                                                                                                                                          laGlyAlaIleLeuGluValCysGly***LysLeuGlyArgPheProGln
                                                                                                                                                                                                                            CAGAGGATGCTGTCAGGAGGAAGCACAATTTGAAACCAAAAAGCTGTATG
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                                                                                                                                                                                                                                                                                                                                                                                              SerCysAspLeuLeuGlyGlnPheAsnLeuLeuGlnLeuAspProAspCy 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATCGGAGGCATGCAGAGAGTTAGGCTTTTCTAGCAACTTGCTTTGCAGC
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98.630
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seq_documentation_block:
ID AAZ43003 standard;
                                            CC AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (EST)
CC sequences, corresponding to human secreted proteins. AAY64651 to
CC AAY65438 represent the EST-related proteins corresponding to AAZ42265 to
CC AAZ43052. The 5' ESTs can be used for producing secreted human gene
CC products. They can be used to identify and isolate 5' untranslated
CC regions (UTRs) and upstream regulatory regions which control the
CC location, development stage, rate, and quantity of protein synthesis, as
CC well as stability of mRNA. The ESTs are also useful as probes for
CC chromosome mapping, and to obtain full length cDNA clones. The ESTs can
CC also be used in forensic procedures to identify individuals, or in
CC diagnostic procedures to identify individuals having genetic diseases
CC resulting from abnormal gene expression. The products may also be used in
CC gene therapy protocols. The nucleic acids encoding signal peptides can be
CC used for directing extracellular secretion of a polypeptide or the
CC insertion of a polypeptide into a membrane, or importing a polypeptide
CC insertion; a variety of human conditions. Secreted proteins have
CC therapeutic value, and the identification of new secreted proteins is
CC valuable. AAZ42249 to AAZ42264 and AAZ4644 to AAZ64650 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               577
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Sequence 623 BP;
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 566-567; 837pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel secreted protein 5' expressed diagnostic, forensic, gene therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-038446/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy; chromosome mapping; upstream regulatory sequence;
forensic; location; development; protein synthesis; stability;
regulation; identification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human 5' EST isolated from a cDNA library SEQ ID NO:762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATCAAGTATGTCCGTGGTTCAGACCCTGTATTAAAGCTTTTGGACGACA 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nIleLysTyrValArgGlySerAspProValLeuLysLeuLeuAspAspA 134
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                                   used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0057719.
98US-0069047.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed sequence tag; secreted protein;
143 A; 120 C;
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182 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence tag sequences used in and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Giordano J;
175
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                                 invention
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alignment_scores

3 other

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seq_documentation_block:
ID AAA16434 standard: |
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                                                                                                                                                                                                                                                                                                 seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:AAA16434
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  Endege WO,
                                           31-AUG-1998;
27-JAN-1999;
                                                                                                                                                                 Colon cancer; de detect mutation;
                                                                            30-AUG-1999;
                                                                                                  09-MAR-2000
                                                                                                                       WO200012702-A2
                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                 Human colon cancer differentially expressed nucleotide sequence
                                                                                                                                                                                                                        14-JUN-2000
                                                                                                                                                                                                                                                                   AAA16434 standard; DNA; 578
                     (FARB ) BAYER CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uLeuLeuAlaThrValLeuGlnAlaValSerAlaPheGlyAlaGluPheS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laGlyAlaIleLeuGluValCysGly***LysLeuGlyArgPheProGln 100
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Ratio:
 Steinmann KE,
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                                                                                                                                                              detect; differential expression; human; treatment;
n; non-invasive diagnostic method; ds.
                                           980S-0098639
990S-0117393
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4.869
85.714
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Gaps: 2
Percent Identity: 85.034
 Astle JH,
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SXCCCCCCCCCCX PX THX RX PH
                                 This sequence represents a human nucleotide sequence which is differentially expressed in colon cancer cells compared to the expression levels in normal cells. The nucleotide sequence can be used as a source of primers and probes. The nucleotide sequence is useful for determining the phenotype of a cell by detecting the differential expression of the sequence relative to a normal cell. The probes derived from the sequence can also be used to determine the phenotype of cells in a sample. Probes and antibodies which hybridise to the nucleotide sequence can also be used to determine the phenotype of a cell. The primers are useful for detecting a mutation in a test nucleotide sequence and also for detecting cancer, preferably colon cancer. Antibodies against the protein encoded by the nucleotide sequence can also be used in a method to detect colon cancer. The diagnostic method is non-invasive and accurate for diagnosing colon cancer at an early stage.
                                                                                                                                                                                                                                                                                                                                          Claim 16;
                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids and useful for treating and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Catino TJ,
Schlegel R;
  Sequence 578 BP;
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143 A;
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102 C; 152
                                                                                                                                                                                                                                                                                                                                      345pp; English.
                                                                                                                                                                                                                                                                                                                                                                             proteins for identifying therapeutic agents diagnosing cancer, especially colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ford
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G; 160 T;
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21 other;
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alignment_block:
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                                                               343
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132 pAsp 133
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                                                                                                                                                                                                                                                                                      ValGlnAlaPheValArgSerAsp.LysProLysLeuPhe...ArgGlyL 116
                                                                                                                      laGlyAlaIleLeuGluValCysGly***LysLeuGlyArgPheProGln 100
                                                                                                                                                     euGlnIleLysTyrVal.ArgGlySerAspProValLeuLysLeuLeuAs 132 ::: |||||||| |||| ||||
                                                                                                                                                                                                 TCTTGTGATCTTCTCGGACAGTTCAACCTGCTTCAGCTGGATCCTGATTG
                                                                                                                                                                                                             SerCysAspLeuLeuGlyGlnPheAsnLeuLeuGlnLeuAspProAspCy
                      CCAAATNAAAGTATGTNNCGTGGTTTCAAACCNTGAATTAAAAGGCTTTT
                                                               GTCCAANCTTTTGTTANGAGTGATAAAACCCAAACTGTTCAGAAGGACTG
                                                                                                          CAGGAGCTATTCTTGAAGTTTGNGGATGAAAATTGGGAAGGTTCCCTNAA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
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4.604
88.235
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Gaps:
Percent Identity:
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86.029
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443 NGAC

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seq_documentation_block:
ID ABL13005 standard; cD
XX
AC ABL13005;
XX
AC ABL13005;
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AC ABL13005;
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AC ABL13005;

XX
Cosophila melanogast
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US-09-676-718A-1 x ABL13005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 33497; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequences (ABL01840-ABL16175) and the (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection
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      18
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                                                                                                                                                                                                                pProAspCysArgGlyCysCysGlnGluGluAlaGlnPheGluThrLysL
ysLeuTyrAlaGlyAlaIleLeuGluValCysGly***LysLeuGlyArg
                                                           GCCTCAGTGTAAGCAATGCTGCACTTTGGATCAGCAGCCGGCGCGCACAGC
                                                                                                                                                                                 ATGTGTTCCAGTTGCGAAAAACTGGATGATTTCGGATTGGATACCATCAA
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2000US-0614150.
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3.659
74.561
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                                                                                                                                                                                                                                                                                                       from:
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Percent Identity:
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seq_name:
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AAF63789 standard;
          This invention relates to polynucleotide sequences AAF63789 - AAF63836 which encode human secreted proteins AAB75280 - AAB75287. Included in the invention are protein sequences AAB75288 - AAB75287 included in the invention are protein sequences AAB75288 - AAB75341 which are fragments of the secreted proteins and amino acid sequences with which these fragments share homology. Examples of the activities of the proteins and polynucleotides and the activities of their agonists and antagonists include, immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; and vulnerary activity. The protein and polynucleotide sequences their accordate and vulnerary activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; autoimmune disease; hyperproliferative disorder; cancer; cardiovascular disorder; cerebrovascular disorder; infection;
                                                                                                                                                                                                                                                                            Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's Parkinson's diseases and cancers -
opthalmalogical; and vulnerary activity. sequences, their agonists and antagonists
                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-071257/08
P-PSDB; AAB75240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2000; 2000WO-US15135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cardiovascular disorder; cerebrovascular disorder; in
nervous system disorder; ocular disorder; chemotaxis;
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                                                                                                                                                                                                                                       Claim 1; Page 440; 530pp;
                                                                                                                                                                                                                                                                                                                                                                                                                        Rosen CA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; immunosuppressive; antiarthritic; antirheumatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME
(ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAGATGCCAGTGGCAAAGTGCAGGAGACGTTGTCCATAACCAAGTGGAAC
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ID ABL13004 standard; cI
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PN W0200171042-A2.
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PF 23-MAR-2000; 2000US-1
PR 11-JUL-2000; 2000US-1
PA (PEKE) PE CORP NY.
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PI Venter JC, Adams M,
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US-09-676-718A-1 x AAF63789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. Included in the invention are oligonucleotides AAF63780 - AAF63788 and peptide AAB75239 which are used in the identification and characterisation of the DNA and protein
                                                                                                                                                                                                                                                                Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster expressed polynucleotide SEQ ID NO 33494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preventing and diagnosing diseases and disorders such as autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders
                                                                                                                                                                                                                                                                                                     pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2002 (first entry)
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                                                                                                                                            23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluPheLeuSerGluLysLeuGluArgIle 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             snIleAlaGluGluLeuSerIleLeuLysTrpAsnThrAspSerValGlu 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sTyrValArgGlySerAspProValLeuLysLeuLeuAspAspAsnGlyA 136
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      Adams M,
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US-09-676-718A-1 x ABL13004/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1278 ATCCGCAGATTCAGGCCTTTATTCAAAGCGGCCGACCTGCCAAGTTCCCC 1229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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                                                                                                                                             Arabidopsis thaliana DNA fragment SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 hrAspSerValGluGluPheLeuSerGluLysLeuGluArg 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2746 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 33494; 21pp + Sequence Listing; English
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279 ATCCTGAAATTGTTGGTTTCATTGAAGAAGAGAAAGAAAAG...TTCCCT
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ID ABA57362 standard;
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30-JUN-2000;
03-AUG-2000;
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2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon nucleic acid probe
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4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98
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US-09-676-718A-1 x ABA57362
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                                                                                                                                                       seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK05398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                           05-NOV-2001
                                                                                                                                                                                                                                                      425
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                                                                                                                                                                                                                                                                                                                                                                               341 TITCTIT......GGCTCCTTCAGCAACTTTCTCTGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                           AAK05398;
                                                                                                      AAK05398 standard;
                                                                                                                                                                                        475 TAGGAGCT 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 GTGGCAGCAGGAGAGTAGATGTCTAGGACTGGCATTTGGGATGCAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 483 BP; 139 A; 91 C; 105 G; 148 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 5667; 639pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                   34 erSerGluAlaCysArgGluLeuGlyPheSerSerAsnLeuLeuCysSer
                                                                                                                                                                                                                   84 laGlyAla 86
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                                                                                                                                                                                                                                                                                                                                                    51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 uLeuLeuAlaThrValLeuGlnAlaValSerAlaPheGlyAlaGluPheS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetalaalaGlyProSerGlyCysLeuValProAlaPheGlyLysArgLe :::||||||||| ||| ||| ||| :::||
                                                                                                                                                                                                                                                     CAGAGAGTACTATCAGAGAAAAGTTCAATTTGAAAACAGAAGCCTGGATG
                                                                                                                                                                                                                                                                     SATGGlyCysCysGlnGluGluAlaGlnPheGluThrLysLysLeuTyrA
                                                                                                                                                                                                                                                                                                                    SerCysAspLeuLeuGlyGlnPheAsnLeuLeuGlnLeuAspProAspCy
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                                           (first entry)
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2.875
69.767
                                                                                                        DNA;
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Gaps: 1
Percent Identity: 51.163
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Human brain expressed single exon

probe SEQ

ID NO: 5389

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alignment_block:
US-09-676-718A-1 x AAK05398
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Quality:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AAK05398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                               375
                                                                                                                                  341
                                                                                                                                                                                       291
                                                                                                                                                                                                                                           241 GTGGCAGCAGAGAGAGTAGATGTCTAGGACTGGCATTTGGGATGCAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single exon nucleic acid probes for analyzing gene expression in human
                          425
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 483 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-483446/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US00667.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; SEQ ID NO: 5389; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                       51
                                                                                                                                                34 erSerGluAlaCysArgGluLeuGlyPheSerSerAsnLeuLeuCysSer 50
                                                                                                                                                                                                                  17
84 laGlyAla 86
                                                     67
                                                                                                                                                                                                                                                         TTTCTTT.....GGCTCCTTCAGCAACTTTCTCTGTTGC
                                                                                                                                                                                    GCCAAGAGCAACTGCATCCCAAGCGCTAGCTGCATTTGGAGCAGTGCTAC 340
                                                                                                                                                                                                               uLeuLeuAlaThrValLeuGlnAlaValSerAlaPheGlyAlaGluPheS 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
; 2000US-0236359.
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2.875
69.767
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                                                                                                                                                                                                                                                                                                                                                                                                                                               91 C;
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Gaps: 1
Percent Identity: 51.163
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                                                                                                                                                                                                                                                                                                                                                                                                                                               G; 148 T; 0 other;
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::|||||| 475 TAGGAGCT 482

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9b_pr: AF26798255
9b_htg: AL355981
9b_pr: AC004925
9b_sts: C25431
9b_sts: G41865
9b_pr: HS74F3F
9b_pr: HS726798251
9b_pr: AF26798251
9b_pr: AF26798251
9b_pr: AF26798251
9b_htg: AP003307
9b_pr: HS74F3R
9b_pr: HS74F3R
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9b_htg: AL355881
9b_pr: AF26798282
9b_pr: HSDJ604K5
9b_htg: AC096112
9b_htg: AC019594
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gb_pat:AX330345
gb_in:AF457547
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9b_pr:BC005294
9b_pr:AF288991
9b_pr:BC016359
9b_ro:AF288740
9b_ro:BC019792
                                                             gb_htg:AC006907
gb_htg:AC096112
gb_pr:AF267982S3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database: GenEmbl:*
Database sequences: 1797656
Database length: 1873333701
Search time (sec): 1928.670000
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                                                                                                                            gb_in:AC024211
gb_in:AC024872
                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_in:AC010054
gb_in:AC009375
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gb_pr:BC021697
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                                                                                                                                                                                                                                                                                                                                                                                                                         gb_in:AE003523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -MODEL-frame+_p2n.model -DEV-x1h
-Q-/cgn2_1/USPTO_spool/USO9676718/runat_17092002_143433_21305/app_query.fasta_1.222
-DB-GenEmbl -QFWT-fastap -SUFFIX-rge -GAPOP-12.000 -GAPEXT-4.000
-MINMATCH-0.100 -LOOPEL-0.000 -LOOPEXT-0.000 -GGAPOP-4.500
-GGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500 -FGAPOP-6.000
-FGAPEXT-7.0050 -XGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
-DELEXT-7.000 -YGAPOP-110.000 -YGAPEXT-0.500 -DELOP-6.000
-DELEXT-7.000 -START-1 -MAYRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -HEAPSIZE-500
-MINLEN-0 -MAXLEN-200000000 -USER-US09676718_eCGN1_1_3896
-NCPU-6 -LOPU-3 -LONGLOG -DEV_TIMEOUT-120 -WARN_TIMEOUT-30
-NO_XLPXY -WAIT -THREADS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sep 18, 2002 5:39
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1.9e-21
1.1e-20
3.0e-20
3.1e-20
3.1e-20
5.3e-20
3.5e-16
1.4e-13
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5.4e-87
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.9e-73
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.6e-06
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.7e-05
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.7e-26
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.7e-24
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.0e-78
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                                                  17201 | ALIZ1989 | Human DNA sequence 17201 | ALIZ1989 | Human DNA sequence 173108 | ACO096112 Rattus norvegicus 173108 | ACO0954 Drosophila melanoga 180787 | ACO09375 Drosophila melanoga 180787 | AECO09375 Drosophila melanoga 180787 | AECO09375 Drosophila melanoga 180787 | ALIZ55981 | Homo sapiens 15 kDa 155871 | ALIZ55981 | Homo sapiens PAC cl 181 | G25431 | human STS EST29806, sequilation of the sequilatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Len
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 | BC021697 Homo sapiens, clone M
10 | BC010481 Mus muscullus, clone I
3 | AX330345 Sequence 854 from Pate
1 | AX457547 Anopheles gambiae sele
165 | AF288992 Homo sapiens 15 kDa
1 | AL55981 Homo sapiens chromo
3 | AF267983 Homo sapiens 15 kDa
t AY043488 Mus musculus selenopro
t BC019742 Mus musculus, clone MC
177 t AL035563 Human DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I AF051894 Homo sapiens 15 kDa s

1 BC005294 Homo sapiens, clone M

1 AF288991 Homo sapiens 15 kDa s

2 BC016359 Homo sapiens clone M

3 I AF288740 Mus musculus 15 kDa s

1 BC019792 Mus musculus, Similar

5 AF305544 Rattus norvegicus 15

1 BC021697 Homo sapiens, clone M

1 BC010481 Mus musculus, clone I
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AUTHORS
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AUTHORS
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ORGANISM
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VERSION
                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS AF051894
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Percent Similarity:
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                                                             uLeuLeuAlaThrValLeuGlnAlaValSerAlaPheGlyAlaGluPheS
  erSerGluAlaCysArgGluLeuGlyPheSerSerAsnLeuLeuCysSer
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98204881
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US-09-676-718A-1 x AF051894
                                                                                    Align seg 1/1 to: AF051894
1244 bp mRNA linear f
Homo sapiens 15 kDa selenoprotein mRNA, complete cds.
AF051894
AF051894.1 GI:3095110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (28-FEB-1998) Department of Biochemistry, University Nebraska, Lincoln, NE 68588, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1244)

Gladyshev, V.N., Jeang, K.T., Wootton, J.C. and Hatfield, D.L.

A new human selenium-containing protein. Purification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 1244)
Gladyshev, V.N., Jeang, K.-T., Wootton, J.C. and Hatfield, D.L.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            characterization, and cDNA sequence
J. Biol. Chem. 273 (15), 8910-8915 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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217 c 257 g 390 t
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98.765
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                                                                                    from:
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Gaps: 0
Percent Identity: 98.765
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121.82
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161951 | AC095199 Rattus norveg
165704 | AC025793 Homo sapiens
1018 | Ac080697 Giardia intesti
783 | AF267985 Homo sapiens 15
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51 i AC095199 Rattus norvegicu
04 i AC025793 Homo sapiens chr
i Ac080697 Giardia intestinal
i AF267985 Homo sapiens 15 kDa
54
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LOCUS BC005294
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                                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nIleLysTyrValArgGlySerAspProValLeuLysLeuLeuAspAspA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ValGlnAlaPheValArgSerAspLysProLysLeuPheArgGlyLeuGl 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGAGGATGCTGTCAGGAGGAAGCACAATTTGAAACCAAAAAGCTGTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATCAAGTATGTCCGTGGTTCAGACCCTGTATTAAAGCTTTTGGACGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_pr:BC005294
                                                                                                     Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 16 Row: b Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 3095110
                                                                                                                                                                                                                                              Dickson, M.,
R. M.
                                                                                                                                                                                                                                                            CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CDNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, web site:

http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens, clone MGC:12358
                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (27-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BC005294.1 GI:13529007 MGC.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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3 IMAGE:4041321,
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1, mRNA,
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                                                              DEFINITION
                                                                                        seq_documentation_block:
LOCUS AF288991
                                                                                                                                                    seq_name:
  VERSION
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SOURCE

KEYWORDS VERSION

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134

355 117 305 101 255

205

67

155

51

FEATURES

gb_pr:AF288991

alternatively spliced.

AF288991

AF288991.1 GI:11138954

Homo sapiens 15 kDa selenoprotein

1519 bp

mRNA

linear

PRI 12-NOV-2000

(SEP15) mRNA,

complete cds;

COMMENT

REMARK

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BASE COUNT
ORIGIN
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                                                                                                                                            381
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                  151 ValGluGluPheLeuSerGluLysLeuGluArgIle
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                                                                                                                                                                               117
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                                                                                                                                                                                                                                                                                    281
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                                                                      181 TCTTGTGATCTTCTCGGACAGTTCAACCTGCTTCAGCTGGATCCTGATTG
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                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                           51 SerCysAspLeuLeuGlyGlnPheAsnLeuLeuGlnLeuAspProAspCy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetAlaAlaGlyProSerGlyCysLeuValProAlaPheGlyLysArgLe
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                                                                                                                                                                                                                                                                                  CAGGAGCTATTCTTGAAGTTTGTGGATGAAAATTGGGAAGGTTCCCTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATCGGAGGCATGCAGAGAGTTAGGCTTTTCTAGCAACTTGCTTTGCAGC
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GTAGAAGAATTCCTGAGTGAAAAGTTGGAACGCATA
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Ratio:
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Gaps:
                                   162
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                                                                                                                uLeuLeuAlaThrValLeuGlnAlaValSerAlaPheGlyAlaGluPheS 34
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                                                                                                                                                                                                                                                    ATGGCGGCTGGGCCGAGTGGGGTGTCTGGGCCGGCGTTTGGGCCTACGGTT
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1 (bases 1 to 1519)

Kumaraswamy,E., Malykh,A., Korotkov,K.V., Kozyavkin,S., Hu,Y., Kwon,S.Y., Moustafa,M.E., Carlson,B.A., Berry,M.J., Lee,B.J., Hatfield,D.L., Diamond,A.M. and Gladyshev,V.N.

Structure-expression relationships of the 15 kDa selenoprotein gene: possible role of the protein in cancer etiology
J. Biol. Chem. 275 (45), 35540-35547 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (21-JUL-2000) Department of Biochemistry, University Nebraska, N151 Beadle Center, Lincoln, NE 68588, USA
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/product="15 kDa selenoprotein"
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AFVRSDKPKLFRGLQIKYVRGSDPVLKLLDDNGNIAEELSILKWNTDSVEEFLSEKLE
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contains SECIS element; selenocysteine"
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/map="1p31"
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/db_xref="taxon:9606"
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Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadanésystemsbiology.org
Anup Madan, Jessica Pahey, Erin Helton, Mark Ketteman, Anuradha
cranhanie Rodrigues, Amy Sanchez and Michelle Whiting
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Homo sapiens, clone MGC:24512 IM
BC016359
BC016359.1 GI:16741016
MGC.
                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LINL at: http://image.linl.gov Series: IRAL Plate: 32 Row: g Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (29-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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/product="Unknown (protein for MGC:24512)"
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/clone_lib="NIH_MGC_54"
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                                                                                                                                    /note="Vector: pDNR-LIB"
                                                                                                                                                                   /lab_host="DH10B"
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Rumaraswamy, E., Malykh, A., Korotkov, K.V., Kozyavkin, S., Hu, Y., Kwnn, S.Y., Moustafa, M.E., Carlson, B.A., Berry, M.J., Lee, B.J., Hatfield, D.L., Diamond, A.M. and Gladyshev, V.N.

Structure-Expression Relationships of the 15-kDa Selenoprotei
                                                                                                                                          Mus musculus 15 kDa selenoprotein AF288740
                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                          Mus musculus
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SNLLCSSCDLLGQFNLLQLDPDCRGCCQEEAQFETKKLYAGAILEVCG"
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alignment_block:
US-09-676-718A-1 x AF288740
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                                                                                                                                                                                                                                                                                                                                                                      uLeuLeuAlaThrValLeuGlnAlaValSerAlaPheGlyAlaGluPheS
                                ValGlnAlaPheValArgSerAspLysProLysLeuPheArgGlyLeuGl
                                                                                                                                                        sArgGlyCysCysGlnGluGluAlaGlnPheGluThrLysLysLeuTyrA
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CAGAGGGTGCTGTCAGGAAGAAGCACAATTTGAAACCAAAAAGCTGTATG
                                                                                                                                                                                                                                                                               CGTCAGAGGCATGCAGAGAGTTGGGTTTCTCCAGCAACTTGCTCTGCAGC
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J. Biol. Chem.
10945981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (21-JUL-2000) Department of Biochemistry, Nebraska, N151 Beadle Center, Lincoln, NE 68588, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kumaraswamy, E., Malykh, A., Korotkov, K.V., Kozyavkin, S., Kwon, S.Y., Moustafa, M.E., Carlson, B.A., Berry, M.J., Lee Hatfield, D.L., Diamond, A.M. and Gladyshev, V.N.
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/gene="Sep15"
/genee"sECIS element; causes positions
be translated as selenocysteine"
a 299 c 341 g 404 t
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SNLLCSSCDLLGQFNLLPLDPVCRGCCQEEAQFETKKLYAGAILEVCGXKLGRFPQVQ
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247. .735
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4.819
95.679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 41 Row: j Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M
Richards, S., Gibbs, R.A.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                          369
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/db_xref="GI:18044684"
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a 243 c 279 g 347 t
                                                                                                                                                                                                                                                    /tissue_type="Mammary tumor. MMTV-LTR/INT3 model. 5 month old mouse. Taken by biopsy." /clone_lib="NCI_GGAP_Mam2" /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                            /note="Vector:
                                                                                                                                                                                                                            pCMV-SPORT6"
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LOCUS AF390544
                                                                                                                                                                                                                                               seq_name: gb_ro:AF390544
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US-09-676-718A-1 x BC019792
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                                             1 (bases 1 to 1236)
Roethlein,D., Kyriakopoulos,A.
A 15 kDa-selenoprotein in seve
                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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           2 (bases 1 to 1236)
Roethlein, D., Kyriakopoulos, A.
                                  Unpublished
                                                                                                                       Rattus norvegicus
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                                                                                                                                                                                              Rattus norvegicus 15
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            and Behne, D
                                                            Behne, D.
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                                                                                                           laGlyAlaIleLeuGluValCysGly***LysLeuGlyArgPheProGln 100
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                                                                                                                                         nIleLysTyrValArgGlySerAspProValLeuLysLeuLeuAspAspA 134
                                                                                                                                                                                                                                                                                      CAGAGGCTGCTGTCAGGAAGAAGCGCAGTTTGAAACCAAAAAGCTGTATG
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| ACTGCTGGCGACTGCGTTTCAAGCGGTGTCTGCTCTTGGGGCAGAGTTCT
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                                                     ACGGGAACATTGCTGAAGAGCTCAGCATCCTCAAGTDDAACACAGACAGT
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4.812
95.062
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1211. .1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="maaggggwlrpaiglrlllatafgavsalgaefsseacrelgfs
snllcsscdliggfnllpldpvcrgccgeeagfetkklyagailevcgxklgrfpgvq
afvrsdkpklfrglqikyvrgsdpvlkllddngniaeelsilkxnvdsveeflsekle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_except=(pos:277. .279,aa:OTHER)
/product="15 kba cytosolic selenoprotein"
/protein_id="Aak73100.1"
/db_xref="G1:14719272"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (11-JUN-2001) SF 6, Hahn-Meitner-Institut, Berlin D-14109, Germany
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LOCUS BC021697
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                       1 MetAlaAlaGlyProSerGlyCysLeuValProAlaPheGlyLysArgLe
  ATGGCGGCTGGGCCGAGTGGGGTGTCTGGTGCCGGCGTTTGGGGCTACGGTT
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                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at http://image.llnl.gov Series: IRAL Plate: 31 Row: o Column: 24
This clone was selected for full length sequencing because it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: CLONTECH Laboratories, In CDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        passed the following selection criteria: Hexamer frequency analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton,
Madan, Stephanie Rodrigues, Amy Sanchez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (14-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: MGC help
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                   400
                                                                                                                        BC021697
                                                                                                                                                                                                                                                                                                                             /product="Unknown (protein for MGC:24367)"
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3 212 c 258 g 379 t
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37, .315
                                                                                                                                                                                     701.50
4.906
87.730
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/clone_lib="NIH_MGC_58"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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/db_xref="taxon:9606"
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IMAGE:4051151, mRNA, complete
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and Michelle Whiting
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17 uLeuLeuAlaThrValLeuGlnAlaValSerAlaPheGlyAlaGluPheS

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Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LINL at: http://image.linl.gov Series: IRAK Plate: 6 Row: b Column: 4
This clone was selected for full length sequencing because it
                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., I
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck,
                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphi
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                             Submitted (10-JUL-2001) National Institutes of Hee Gene Collection (MGC), Cancer Genomics Office, Natinstitute, 31 Center Drive, Room 11A03, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus, clone IMAGE:3482046, BC010481
                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                       Muzny, D.M.,
                                                                                                                                                                        Center code: BCM-HGSC
                                                                                                                                                                                           Sequencing Center
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partial cds.
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National Cancer
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ı, W.,
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     TITLE
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seq_documentation_block: LOCUS AX330345
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                                                                                                                                                                                                                                                                                                                                                                    135 yAsnīleAlaGluGluLeuSerīleLeuLysTrpAsnThrAspSerValG 152
                                                                                                                                                                                                                                                                                                                     152 luGluPheLeuSerGluLysLeuGluArgIle
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                                                                                                                                                                                                                                                                                                                                                        AAGTATGTTCGAGGCTCAGACCCTGTACTAAAGCTTTTGGACGACAACGG
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Young, P.E., Augustus, M., Carter, K.C., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeu
                                                                                                                                                                  Sequence 854 from AX330345
                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                    AX330345.1 GI:18103323
                                                                                                      Homo sapiens
                                                     (sites)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="Unknown (protein for IMAGE:3482046)"
/protein_id="AaH10481.1"
/db_xref="G1:14714680"
/translation="GAVKKHNLKPKSCMQEPSLKSADENWGGSLKSKLLSEVINPNS
SEVYRSSMFEAQTLY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Mammary tumor.
old, gross tissue."
/clone_lib="NCI_CGAP_Mam5"
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5.118
98.936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
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                                                                                                                                                                                    Patent
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                                                                Craniata; Vertebrata; Catarrhini; Hominidae;
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     therapeutic
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                                  Ebner, R.,
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US-09-676-718A-1 x
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                                                                                                                                                                                                                                                                                                                                                                      gb_in:AF457547
                                                                                                                                                                                     Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene sets
Patent: WO 0194629-A 854 13-DEC-2001;
Avalon Pharmaceuticals (US)
Location/Qualifiers
Submitted (12-DEC-2001) Section of Medical Entomology/Laboratory of Parasitic Diseases/NIAID, National Institutes of Health, 4 Center Drive, Building 4, Room 126, MSC 0425, Bethesda, MD 20892-0425, USA
                                                                                                          Francischetti, I.M., Valenzuela, J.G. and Ribeiro, J.M.
Towards a catalog for genes and proteins from the salivary
the malaria vector, Anopheles gambiae
                                                                                                                                                                                                                                                                                            Anopheles gambiae selenoprotein mRNA, AF457547
                                            Francischetti, I.M., Valenzuela, J.G. and Ribeiro, J.M. Direct Submission
                                                                                                                                                            Culicoidea; Anopheles.
1 (bases 1 to 624)
                                                                                                                                                                                                                                                                            AF457547.1 GI:18389880
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                                                                                           Unpublished
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/db_xref="taxon:9606"
61 c 92 g 9
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                                                                                                    AATGGAACACCGACACGGTGCAGGAGTTTTTCGAAACACGTTTGGCGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGAAAGAGCATTGCCTAGAATGTTGCCCAAAAGGACACTGAAGCCGATTC
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seq_documentation_block:
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DEFINITION

Homo

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PRI 12-NOV-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kumaraswamy, E., Malykh, A., Korotkov, K.V., Kozyavkin, S., Hu, Y., Kwon, S., Moustafa, M.E., Carlson, B.A., Berry, M.J., Lee, B.J., Hatfield, D.L., Diamond, A.M. and Gladyshev, V.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hatfield,D.L., Diamond,A.M. and Gladyshev,V.N. Structure-Expression Relationships of the 15-kDa Selenoprotein Gene. POSSIBLE ROLE OF THE PROTEIN IN CANCER ETIOLOGY J. Biol. Chem. 275 (45), 35540-35547 (2000)
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Lee,B.J.,
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REFERENCE
AUTHORS
TITLE
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SOURCE
ORGANISM
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                                                                                                   COMMENT
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LOCUS AL355981
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                                                                                                                                                          JOURNAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..LysProLysLeuPheArgGlyLeuGlnIleLysTyrValArgGlySer 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnPheGluThrLysLysLeuTyrAlaGlyAlaIleLeuGluValCysGl 92
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Ratio:
                                                      Center: Sanger Centre
                                                                                             Submitted (21-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 128, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 12, 2000 this sequence version replaced gi:9213687.
                                                                                                                                                                                                                                                                                                                                                                  AL355981 15871 bp DNA 1.
Homo sapiens chromosome 1 clone RP11-277G24,
PROGRESS ***, 15 unordered pieces.
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                    AL355981
                                        Center code:
                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                            Direct Submission
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4, *** SEQUENCING IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert size: 154471; sum-of-contigs
Insert size: 176463; 14.5% error; agarose-fp
Quality coverage: 3.58x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: bA277G24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98427 98526: gap of 100 bp 98527 106876: contid of 8350 bp in length 106877 106976: gap of 100 bp 106977 111928: contid of 4952 bp in length 11929 112028: gap of 100 bp 119408: contid of 7380 bp in length 119409 119508: gap of 100 bp 119509 137994: contid of 18486 bp in length 137995 138094: gap of 100 bp 137995 142132: contid of 18486 bp in length 142133 142232: gap of 100 bp 
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15248 15347: gap of 100 bp
15348 21318: contig of 5971 bp in length
21319 21418: gap of 100 bp
21419 25399: contig of 3881 bp in length
25300 25399: gap of 100 bp
25400 30376: contig of 4977 bp in length
30477
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149041 155871: contig of
Location/Qualifiers
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fragment_chain:1"
                               note-"assembly_fragment:00232
                                                                                                                                                                                    note="assembly_fragment:00125"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72896:
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1904
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98426: cont
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                                                                                                                                                         .33263
       .98426
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of 2787 b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39433 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in length
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FEATURES

DEFINITION

Homo sapiens 15 AF267983

kDa selenoprotein

gene, exon DNA

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seq_documentation_block:
LOCUS AF267982S2
                                                                    seq_name: gb_pr:AF267982S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AL355981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-676-718A-1 x AL355981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                          39034
                                                                                                            39110 AGAAG 39114
                                                                                                                                                                                   39060 CAACTGATTTCTTGTCTGGCCTATTAGTTCAATCAAAGCAAATATGAAGG
                                                                                                                                                                                                                                                                                                                                38990 AAAAATGTAAGTTGCTTAAT.....CAATTTAAGTGTAAAAAAAGCCTCT 39033
                                                                                                                                                                                                                                                                                                                                                                                                           38956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38820 CTTTTCTAGCAACTTGCTTTGCAGCTCTTGTGATCTTCTCGGACAGTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38770 GTGTCTGCTTTTGGGGCAGAGTTTTCATCGGAGGCATGCAGAGAGTTAGG
                                                                                                                                                                                                                         141
                                                                                                                                                                                                                                                                                                125
                                                                                                                                                                                                                                                                                                                                                               109 ..LysProLysLeuPheArgGlyLeuGlnIleLysTyrValArgGlySer 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 yPheSerSerAsnLeuLeuCysSerSerCysAspLeuLeuGlyGlnPheA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 ValSerAlaPheGlyAlaGluPheSerSerGluAlaCysArgGluLeuGl
                                                                                                                                                 luLys 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnPheGluThrLysLysLeuTyrAlaGlyAlaIleLeuGluValCysG1 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         snLeuLeuGlnLeuAspProAspCysArgGlyCysCysGlnGluGluAla
                                                                                                                                                                                                                   uSer...IleLeuLysTrpAsnThrAspSerValGluGluPheLeuSerG
                                                                                                                                                                                                                                                                                                                                                                                                                                       y***LysLeuGlyArgPheProGlnValGlnAlaPheValArgSerAsp. 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAATTTGAAACCAAAAAGGTACTGTTTTCTAGTATA......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCTGCTTCAGCTGGATCCTGATTGCAGAGGATGCTGTCAGGAGGAAGCA
                                                                                                                                                                                                                                                                                          AspProValLeuLysLeuLeuAspAspAsnGlyAsnIleAlaGluGluLe 141
                 AF267982S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
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3.102
72.593
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98527. .106876
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31293 c 31116 g 47497 t 1
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/note="assembly_fragment:01243"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment:00503"
119509. .137994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="assembly_fragment:00752"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="assembly_fragment:00572"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="assembly_fragment:00459"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="assembly_fragment:00437"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="assembly_fragment:01162"
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Gaps: 6
Percent Identity: 54.815
                 1743 bp
                                                                                                                                                                                                                                                          ... CATTTTTTAGTAAAACT
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linear
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                 PRI 27-JUN-2000
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REFERENCE
AUTHORS
TITLE
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SOURCE
ORGANISM
                                                              VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-676-718A-1 x AF267982S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                  SOURCE
                                                                                                                                                                 DEFINITION
                                                                                                                                                                                seq_documentation_block:
LOCUS HSDJ604K5
                                                                                                                                                                                                                          seq_name: gb_pr:HSDJ604K5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    995
                                                                                                                                                                                                                                                                                                                           945
                                                                                                                                                                                                                                                                                                                                                                                           895
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                                                                                                                                                                                                                                                                                                                                                         76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91
                                                                                                                                                                                                                                                                                           sGly
                                                                                                                                                                                                                                                                                                                         GlnPheGluThrLysLys...LeuTyrAlaGlyAlaIleLeuGluValCy 91
                                                                                                                                                                                                                                                                                                                                                                                                        snLeuLeuGlnLeuAspProAspCysArgGlyCysCysGlnGluGluAla 75
                                                                                                                                                                                                                                                           TGGT 998
                                                                                                                                                                                                                                                                                                                                                                                       ACCTGCTTCAGCTGGATCCTGATTGCAGAGGATGCTGTCAGGAGGAAGCA 944
                                                                                                           Human DNA sequence from clone RP4-604K5 on chromosome 1p22.2-31.1. Contains a gene for a 15 kba selenoprotein and a part of the heparan sulfate 2-sulfotransferase gene (KIAAO448). Contains ESTs, STSs, GSSs and CpG islands, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
 Eukaryota; Metazoa; Mammalia; Eutheria;
                                                              AL121989.12 GI:8919105
HTG; CpG island; KIAA0448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The human 15-kDa selenoprotein gene : Characterisation of the genomic structure and functional analysis of the promoter
                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-MAY-2000) Biological Science, Wonchun-dong, Paldal-gu, Suwon, Kyungki-do 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1743)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ryu, M. and Moon, E. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ryu, M. and Moon, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of 5
                                                                                                                                                                                                                                                                                         92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 1743)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303.50
4.742
94.118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2075D19"
795...962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /number-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:8745559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 68
Gaps: 1
Percent Identity: 86.765
 Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1 to: 1743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               342 g
                                                                                                                                                                            127201 bp
                                                              selenoprotein;
Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 540 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 others
                                                               sulfotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Ajou University, San-5, 442-749, South Korea
               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
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                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                         repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VECTOR: PCYPAC2
                                                                                                                                                                           /note="AluSc repeat: matches 1. 2839. .2962
                                                                                                                                                                                                                                                                       2021. .2070
/note="Alu repeat: matches 253.
2138. .2181
                                                                                                                                                                                                                                                                                                     /note="MIR repeat: matches 117. 2021 . 2070
                                                                                                                                                                                                                                                                                                                                     /note="Alux repeat: matches 1. 1951. .1982
             /note="match: GSS: Em:AQ697506" 4591. .4712
                                             /note-"match: 3668. .4152
                                                                                                                                                                                                                                                                                                                                                                                                        874. .1348
                                                                             /note="match: 3657. .4233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /map="p22.2-31.1"
/clone="RP4-604K5"
/clone_lib="RPCI-4"
                                                                                                                        /note="AluSp repeat: matches 4.
                                                                                                                                                      2839. .2962
/note="MIR repeat: matches 20.
                                                                                                                                                                                                                                                                                                                                                                                      /note="match: GSS: Em:AQ432443"
                                                                                                                                                                                                                                                                                                                                                                                                                     /note="L1MC4 repeat: matches 7888. .7977 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="L1MC4 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MLTID repeat: matches 113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
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L2 repeat:

matches 2582.

. 2693

of.

consensus" consensus"

.170 of consensus"

.302 of consensus

.287 of consensus*

GSS: .3650

Em: AQ376380* Em: AQ204224

matches 2575.

.2710

of.

consensus"

L2 repeat: matches 2648.

.2691 of

matches 7364.

. 7597

of consensus"

.504 of consensus*

.299 of consensus"

.302 of consensus" .148 of consensus

```
feature key.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: KMRL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1

RP4-604K5 is from the library RPCI-4 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 5, 2000 this sequence version replaced g1:8894634.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                    This sequence is the entire insert of clone RP4-604K5
Location/Qualifiers
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organism="Homo sapiens"
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repeat_region
                                                                                                                        /note="AluSc repeat: matches 5..30: 15709..16030
/note="MLT1B repeat: matches 109... 16038..16338
/note="L2 repeat: matches 1316..16: complement(16360..16819)
/note="match: GSS: Em:A0474120"
complement(16396..16819)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13024. .13195

/note="L2 repeat: matches 1439. .1596 of consensus 13196. .13505

/note="Alusq repeat: matches 1. .309 of consensus" 13506. .13644

/note="L2 repeat: matches 1260. .1439 of consensus complement(13824. .14267)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Alux repeat: matches 137. .303 of consensus"
10040. .10267
/note="L2 repeat: matches 2524. .2747 of consensus"
/note="L2 repeat: matches 2524. .2747 of consensus"
10491. .10777
/note="AluSp repeat: matches 1. .288 of consensus"
/note="AluSp repeat: matches 1. .288 of consensus"
/note="match: GSS: Em:847699"
complement(10926. .11344)
/note="match: GSS: Em:AQ240745"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9437. .9569
/note="AluY repeat: matches 3.
9570. .9867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5034. 5114
/note="LTR33 repeat: matches 425. .516 of consensu: 5135. 5447
/note="Rhlusq repeat: matches 1. .313 of consensus" 5636. 5822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="match: GSS: Em:AQ549616"
12369. .1266
/note="Alusx repeat: matches 1. .300 of consensus"
complement(12390. .12881)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9868. .10039
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6670. .6805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluY repeat: matches 1. 6258. .6562
  /note="AluSx repeat: matches 1.
17557. .17734
                                          /note="L2 repeat: matches 1674.
17101. .17411
                                                                                                                                                                                                                                                                                                                                         /note="MIR repeat: matches 22. .191 of consensus" 14808. 15098 rote="Alusg repeat: matches 1. .291 of consensus" 15315. .15407
                                                                                                                                                                                                                                                                                                                                                                                                                                14377. .14548
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11010. .11339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="match: GSS: Em:AQ385701"
10964. .11765
                                                                                                                                                                                                                                                                                                 /note="MLT1B repeat: matches 10.
15408. .15708
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="match: GSS: Em:AQ233950"
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7619. .7813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5636. .5822
note="ITR33 repeat: matches 9. .206 of consensus"
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                                                                                                      note="match: GSS: Em:AQ469284"
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.9365
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                                                                                                                                                                                                                                                                           .305 of consensus"
                      .312 of consensus"
                                                            .1816 of consensus
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70741

70691 TGGT 70688

sGly 92

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alignment_block:
US-09-676-718A-1 x HSDJ604K5/rev
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Ratio:
Percent Similarity:
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GlnPheGluThrLysLys...LeuTyrAlaGlyAlaIleLeuGluValCy 91
                                                                               snLeuLeuGlnLeuAspProAspCysArgGlyCysCysGlnGluAla 75
                                                                                                                                                                yPheSerSerAsnLeuLeuCysSerSerCysAspLeuLeuGlyGlnPheA
                                                           ACCTGCTTCAGCTGGATCCTGATTGCAGAGGATGCTGTCAGGAGGAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MER30 repeat: matches 125. .223 of consensus" 22932. .23242
/note="AluSq repeat: matches 1. .311 of consensus" 23252. .23300
/note="MLT1G repeat: matches 443. .506 of consensus" 23477. .23777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MLT2FA repeat: matches 17. .391 of consensus" 21123. .21418
/note="AluSq repeat: matches 1. .297 of consensus" 21688. .22106
/note="MLT1G repeat: matches 10. .423 of consensus" 22107. .22383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22107. .2283
/note="AluJo repeat: matches 13. .
22384. .22405
/note="MLTIG repeat: matches 423.
22406. .22532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="AluJb repeat: matches 1. .297 of consensus 20143. .2038 // 20145. .2038 // 20145. .20318 // 20145. .20913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MER5A repeat: matches 1. .34 of consensus" 17773. .18080
/note="Alux repeat: matches 1. .306 of consensus" 18081. .18252
/note="MER5A repeat: matches 34. .189 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="L2 repeat: matches 1995.
17741. .17772
                                                                                                                                                                                                                                                                                                                                                                                                           303.50
4.742
94.118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="L1MA3 repeat: matches 5992. .6105 of consensus"
24821. .25108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="AluSg repeat: matches 1. .307 of consensus"
24702. .24820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Alusx repeat: 24394. .24690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MER30 repeat: matches 1. 22533 . 22841 . /note="Alux repeat: matches 1. . 22842 . . 22931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluSp/q repeat: matches 201. .311 of consensus"
19609. 19843
/note="MSTA repeat: matches 198. .426 of consensus"
19844. .20142
                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Gaps:
Percent Identity:
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1
86.765
                                                                                                                                                                                                                                                                                                       to: 127201
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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    55
66
77
110
111
113
114
115
                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   311
250.5
226.5
81
76.5
76.5
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                                                                                                                                                                                                                                                                                                        SPTREMBL_19:*

1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organe1.
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
11: sp_rodent:
12: sp_virus:*
13: sp_virus:*
13: sp_virus:*
14: sp_unclass
15: sp_archeap
17: sp_archeap
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Match Length
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831
1 MAAGPSGCLVPAFGKRLLLA.....ILKWNTDSVEEFLSEKLERI 162
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                                                                                                                                                                                                                                                                                                        sp_unclassified:*
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sp_rodent:*
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                                                                                                                                                                                                                                     SUMMARIES
O9gzwO homo sapien
O9err7 mus musculu
O92378 rattus norv
O9bs64 homo sapien
O9vv)7 drosophila
O9n4c6 caenorhabdi
O9sy13 arabidopsis
O22639 glyvine max
O9vqe9 drosophila
O94594 leishmania
O39830 glyvine max
P73692 synechocyst
O94785 trypanosoma
O93929 trypanosoma
O93929 trypanosoma
O93929 trypanosoma
O93929 trypanosoma
O93939 trypanosoma
O94785 trypanosoma
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094667 s	0	560	8 . 5	71	5
Q9zpr	10 Q9ZPR4			71	4
Q9vcx2	5 Q9VCX2		•	71.5	43
Q9xyx8	_		8.6	71.5	42
Q9ngq0	5 Q9NGQ0		8.6	71.5	41
90du6Q	5 Q9UB06		8.6	71.5	40
Q9gyw3	5 Q9GYW3		8.6	71.5	39
Q91gx9	10 Q9LGX9		8.6	71.5	38
076958	٥	514	8.6	71.5	7
Q94f41	10 Q94F41	500	8.6	71.5	5
Q9n6x2	o	432	8.6	71.5	5
Q9m0x6 arabidopsis	10 Q9M0X6	777	8.7	72	4
Q9m4e8	10 Q9M4E8	665	8.7	72	$\ddot{\omega}$
Q9ngm4	ဂ		8.7	72	ວ
060996	5 060996		8.7	72	31
Q01678	٥		8.7	72	30
Q9lyn8 arabidopsi			8.7	72.5	õ
Q95qy9	٥	838	8.7	72.5	æ
		838	8.7	72.5	7
Q93176 caenorhabdi	5 Q93176	830	8.7	72.5	9
Q91e55	0	762	8.7	72.5	ŭ
Q95y00	5 Q95Y00	205		72.5	4
023248	10 023248	274		73	ũ
Q9m2u5	10 Q9M2U5	273	٠	73	Ñ
073774	13 073774	704	9.0	74.5	ï
Q941k4	10 Q94IK4	665		74.5	õ
0yeeeQ	12 Q993Y0	456	9.0	75	ف
Q26937 trypanosoma	5 Q26937	678	9.1	75.5	œ
Q26936	5 Q26936	653	9.1	75.5	7

## ALIGNMENTS

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Фр	Ma Ma	ŏ	DR	RE	RT	3 2	8	RA	æ	RP	RN	RL	RA A	RΡ	RN	×	გ	ద	S	GN	DE	DT	DŢ	Ŋ	AC	ij	09GZW0	RESULT
1 MAAGPSGCLVPAFGKRLLLATVLQAVSAFGAEFSSEACRELGFSSNLLCSSCDLLGQFNL 60 	Query Match 98.9%; Score 822; DB 4; Length 162; Best Local Similarity 99.4%; Pred. No. 6.4e-79; Matches 161; Conservative 0; Mismatches 1; Indels 0; Gaps (	SEQUENCE 162 AA; 17750 MW; 5B94FBB423A089EE CRC64;	EMBL; AF288991; AAG31556.1;	J. Biol. Chem. 275:35540-35547(2000).	POSSIBLE ROLE OF THE PROTEIN IN CANCER ETIOLOGY.";	Hattield D.L., Diamond A.M., Gladyshev V.N.,	Kwon S.Y., Moustafa M.E., Carlson B.A., Berry M.J., Lee B.J.,	Kumaraswamy E., Malykh A., Korotkov K.V., Kozyavkin S., Hu Y.,	PubMed=10945981;	SEQUENCE FROM N.A.		Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.	Pearce A.;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=9606;		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens (Human).	DJ604K5.1 OR SEP15.	15 KDA SELENOPROT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)	16,	01-MAR-2001 (TrEMBLrel. 16, Created)	Q9GZWO;	Q9GZWO PRELIMINARY; PRT; 162 AA.	WO	ILT 1
	0;																											

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RA KWON S.Y., MOUSTATA M.E., CARISON B.A., Berry M.J.,
RA Hatfield D.L., Diamond A.M., Gladyshev V.N.;
RT "Structure-Expression Relationships of the 15-kDa Sel
RT POSSIBLE ROLE OF THE PROTEIN IN CANCER ETIOLOGY.";
RL J. Biol. Chem. 275:35540-35547(2000).

RR EMBL; AF288740; AAG31765.1; -.

R MGD; MGI:1927947; Sep15.
         REPARATE TO SERVICE TO
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01-MAR-2001
01-DEC-2001
15 KDA SELEN
SEQUENCE FROM N.A.

Roethlein D., Kyriakopoulos A., Behne D.;

Roethlein D., Kyriakopoulos A., Behne D.;

*A 15 kDa-selenoprotein in several tissues of Submitted (JUN-2001) to the EMBL/GenBank/DDBJ EMBL; AF390544; AAK73100.1; -.

SEQUENCE 162 AA; 17706 MW; 65E939968C8B721
                                                                                                                                                                                                                                                              Q923V8;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQLDPDCRGCCQEEAQFETKKLYAGAILEVCGXKLGRFPQVQAFVRSDKPKLFRGLQIKY
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Rodentia;
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Pred. No. 2.5e
1; Mismatches
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Last sequence update)
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                                                                                                                                                                                           Craniata; Vertebrata;
Sciurognathi; Muridae
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           65E939968C8B72AC CRC64;
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2.5e-71;
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Lee
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; Murinae; Rat
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В.J.,
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O9BS64;

O9BS64;

O1-JUN-2001 (TrEMBLrel. 17, Created)

O1-JUN-2001 (TrEMBLrel. 17, Last sequence upon the control of 
                                                                                                                  Q9VVJ7; PRELIMINARY;
Q9VVJ7;
01-MAY-2000 (TIEMBLITEL 1
01-MAY-2000 (TIEMBLITEL 1
01-MAY-2000 (TIEMBLITEL 1
CG7484 PROTEIN.
CG7484 PROTEIN.
CG7484 PROTEIN.
                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; H
Pterygota; Neoptera; Endopterygota; Diptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein. SEQUENCE 92 AA; 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
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Strausberg R.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAAGPSGCLVPAFGKRLLLATVLQAVSAFGAEFSSEACRELGFSSNLLCSSCDLLGQFNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAAGPSGCLVPAFGKRLLLATVLQAVSAFGAEFSSEACRELGFSSNLLCSSCDLLGQFNL
                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQLDPDCRGCCQEEAQFETKKLYAGAILEVCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAAGPSGCLVPAFGLRLLLATVLQAVSAFGAEFSSEACRELGFSSNLLCSSCDLLGQFNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQLDPDCRGCCQEEAQFETKKLYAGAILEVCGXKLGRFPQVQAFVRSDKPKLFRGLQIKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAAGQGGWLRPALGLRLLLATAFQAVSALGAEFSSEACRELGFSSNLLCSSCDLLGQFNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EC016359; AAH16359.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPLDPVCRGCCQEEAQFETKKLYAGAILEVCGXKLGRFPQVQAFVRSDKPKLFRGLQIKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQLDPDCRGCCQEEAQFETKKLYAGAILEVCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MAR-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s (Human).

Metazoa; Chordata; C
Metazoa; Primates; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                  Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADENOCARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9669 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHRONIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.5%;
92.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.0%;
98.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                 13,
13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 68;
                                                                                                                                                                                                              Created)
Last sequential Last annotation
                               Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYELOGENOUS LEUKEMIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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Pred. No. 1.1e-70;
0; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 474; DB 4;
Pred. No. 1.7e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59EABAD5F7FAAD58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                 sequence up
annotation
                                                                                                                                                                                                                                                                                                                                             142
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                                                                                        Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                               Brachycera;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                            Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                  Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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RESULT
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler H., Caddleu E., Center A., Chandra I.,
RA de Pablos B., Delcher A., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.M., Li J., Li Z., Liang Y., Lin X.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.M., Li J., Li Z., Liang Y., Lin X.,
RA Meltulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Rainert K.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Williams S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Hoodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Hoodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Pheng X.H., Zhong F.N., Zhong W., Zhon W., Zhong S., Zhao Q., Zheng L.,
RA Globs R.A., Myers E. W., Rubin G.M., Venter E., Wang A.H., Wang Y.,
RA Williams S.M., Worley S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Sheng Y. L., Raishin G.M., Venter J.C.,
RA Sheng Y. L., Raishin G.M., Venter J.C.,
RA Sheng Y. L., Raishin G.M., Venter J., She
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Q9N4C6;
Q9N4C6;
T01-OCT-2000 (TrEMBLrel. 15, Created)
T01-OCT-2001 (TrEMBLrel. 18, Last sequence updated)
O1-DEC-2001 (TREMBLrel. 19, Last annotation uporterical 17.6 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local
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                          Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GRPAKFPNIQIKYVRGLDPVVKLLDASGKVQETLSITKWNTDTVEEFFETHLAK 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LCSSCDLLGQFNLLQLDPDCRGCCQEEAQFETKKLYAGAILEVCGXKLGREPQVQAFVRS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKPKLFRGLQIKYVRGSDPVLKLLDDNGNIAEELSILKWNTDSVEEFLSEKLER 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MCSSCEKLDDFGLDTIKPQCKQCCTLDQQPAAQRTYAKAILEVCTCKFRAYPQIQAFIQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                          Nematoda; Chromadorea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 311;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                      sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.6e-25;
                                                        Rhabditida; Rhabditoidea;
                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 142,
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C STRAIN-CV. COLUMBIA;

(C STRAIN-CV. COLUMBIA;

(C STRAIN-CV. COLUMBIA;

(A) Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,

(A) Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,

(A) Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,

(B) Conzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,

(B) Conzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,

(B) Conzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,

(B) Conzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,

(B) Conzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,

(B) Conzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,

(B) Conzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,

(B) Conzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,

(B) Conzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,

(B) Conzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,

(B) Conzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,

(B) Conzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,

(B) Conzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,

(B) Conzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,

(B) Conzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,

(B) Conzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,

(B) Conzalez A., Kremenetskaia I., Kim C., Lenz C., Liu J., 
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O9SYL3;

O1-MAY-2000 (TrEMBLrel. 1

O1-MAY-2000 (TrEMBLrel. 1

O1-JUN-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Submitted (SEP-2001) to the
EMBL; AC024211; AAF36064.2;
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SEQUENCE 152 AA; 17593 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BRISTOL N2;
MEDLINE-99069613;
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SEQUENCE FROM N.
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Pred. No. 1.2e-18;
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No. 4.3e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosida eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
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-I- SIMILARITY: BELONGS TO THE HEAT SHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Water-stress regulation and molecular analysis of the soybean gene family.":
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Eukaryota; Viridiplantae;
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                                                                                                                                                                                                                                                                   PRNTVIPT -- KKSQVFTTYQDQQTTVSIQVFEGERS---
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                                                                     SQEETERMVREEKDFAEEEKKVKERIDARNSLETYVYNMKNQVSDKDKLADKLE
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(TremBirel. 05, Last sequence update)
(TremBirel. 19, Last annotation update)
RETICULUM HSC70-COGNATE BINDING PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            Score 81; I
Pred. No. 5.
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ENDOPLASMIC RETICULUM HSC70-COGNATE
BINDING PROTEIN.
                                                                                                                                                                    -ANGILNVKAEDKGTGKSEKITITNEKGRL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A2020A7DC1A0B0BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160
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                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                       DB
5.5;
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                                                                                                                                                                                                                                                                                                                                                                     62;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 668;
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                      -LTKDCRLLGKF 490
                                                                                                                                                                                                                                                                                                                                                                     50;
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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Man K.H., Doyle C., Boyers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Man L.J. F., Agbayani A., An H.J., Andrews-Pfannkoch C., Beldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Glods R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun P.,
RA Glods R., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.,
RA Glods R., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lina Y., Lin X.,
RA Halstov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Woy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb JM.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb M.,
RA Nelson D.R., Nelson K.A., Sanders R.D.C., Scheeler F., Smeh H.,
Shue B.C., Stapleton M., Strong R., Sun E.,
RA Sheng X.H., Zhong W., Routy J.S., Jan X., Jan S., Pacleb JM.,
RA Sheng X.H., Zhong W., Routy J.S., Jan X., Smith T.,
RA Sheng K.H., Routy J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Sheng X.H., Zhong W., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Sheng R. Hall M. R., Routy J.S., Sheng S.
                                                                                                               Matches
                                                                                                                                  Query Match
Best Local
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Q9VQE9
01-MAY-2000 (TFEN
01-MAY-2000 (TFEN
01-JUN-2001 (TFEN
CG11542 PROTEIN
CG11542.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Neoptera; Endopteryota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                        FlyBase; FBgn0031447; CG11542.
InterPro; IPR001440; TPR.
Pfam; PF00515; TPR; 1.
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                                       151
   78
                                                                            18
 ETKKLYAG-AILE---VCGX--KLGRFPQVQ-AFVRSDKP
                                                                          LLATVLQAVSAFGAEFSSEACRELGFSSNLLCSSCDLLGQFNLLQLDPDCRGCCQEEAQF
                                                                                                               . Similarity 27; Conserv
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                                                                                                                 Conservative
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                                                                                                                                                                                                 57320 MW;
                                                                                                                              9.3%;
                                       --- LCKETAITALLLCGLCDVLSPVGRENSDKVCDGSISGLASF
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                                                                                                             Score 77; DB Pred. No. 11; 17; Mismatches
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                                                                                                                                                                                                          BABA560198C3E6DA CRC64;
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                                                                                                               42;
                                                                                                                                              Length 523
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.A., Galle R.E
                                                                                                               Indels
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204 NFQRRFRSLSILGFTLLCGLYCRLSLLPRPSTAFSAADNP

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RESULT

ID 929

ID 929

AC Q2

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D7 01

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Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996
01-NOV-1996
01-DEC-2001
SEQUENCE FROM N.A.

STRAIN-LEM75 /ZYMODEME 1;

MEDLINE-96352058; PubMed-8728991;

Quijada L., Requena J.M., Soto M., Alonso C.;

Quijada L., Requena J.M., Soto M., Alonso C.;

Quijada L., Requena J.M., Soto M., Alonso C.;

Puring canine viscero-cutaneous leishmaniasis the antibodies are specifically elicited by the parasit parasitology 112:277-284(1996).

1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 7

EMBL; X85799; CAA59793.1; -.

EMBL; X85799; CA559793.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Q25292
Q25292;
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PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01336; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Y08020; CAA69282.1; -. EMBL; Y08019; CAA69281.1; -. HSSP; P08107; 1HJO.
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01-FEB-1997 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
HEAT SHOCK PROTEIN 70.
                                                                                                                                                                                                                                                  Leishmania infantum.
Eukaryota; Euglenozoa;
NCBI_TaxID=5671;
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Quijada L., Soto M., Alonso C., Requena J.M.;
"Analysis of post-transcriptional regulation operating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Euglenozoa; NCBI_TaxID=5671;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transcription products of the tandemly linked Leishmania infantum
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Biol. Chem. 272:4493-4499(1997).
SIMILARITY: BELONGS TO THE HEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MTKDCHLLGTFDLSGIPPAPRGLPQIEVTFD---LDANGILNVSABEKGTGKRNQITITN
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(TrEMBLIE).
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Last sequence up
Last annotation
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Pred. No. 16;
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                                                SHOCK PROTEIN 70 FAMILY.
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                                                                                        parasite
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                                                                                                              anti-Hsp70
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Best Local S
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Best Local S
Matches 24
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Q39830;
01-NOV-1996
                                                                                                                                                                                                                                                                                 PROSITE; PSO
ATP-binding.
                                                                                                                                                                                                                                                                                                                                              PROSITE;
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Pfam; PF0(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=CENTURY 84; TISSUE=LEAF;
MEDLINE=95218610; PubMed=7766051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosiceurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BIP ISOFORM A. Glycine max (Soybean).
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PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
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01-DEC-2001
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InterPro; IPR000671; Hydrgn_uptake
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                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00301; HEATSHOCK70
                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00012; HSP70;
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                                          59
                                                                                                                                                                                Local Similarity
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  ELSGIPPAPRGTPQIEVTFEVD--
                                     NLLQLDPDCRGCCQEEAQFETKKLYAGAILEVCGXKLGRFPQVQAFVRSDKPKLFRGLQI 118
                                                                             PRNTVIPT - - KKSQVFTTYQDQQSTVSIQVFEGERS
                                                                                                                   PSGCLVPAFGKRLLLATVLQ-----AVSAFGAEFSSEACRELGFSSNLLCSSCDLLGQF
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PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                           PS00014; ER_TARGET; PS00297; HSP70_1; 1.
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0012; HSP70; 1.
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                                                                                                                                                                                                                                                              664 AA;
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Pred. No. 16;
26; Mismatches
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01-FEB-1997
01-JUN-2001
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EMBL; D90908; BAA17739.1; --
INTERPO; IPRO01440; TPR.
Hypothetical protein; Complete proteome.
SEQUENCE 265 AA; 29760 MW; 3A344CF7BDC25569 CRC64;
                     Tanaka M.,
"The parasi
                                                                                                                                    Trypanosoma cruzi.
Eukaryota; Euglenozoa;
NCBI_TaxID=5693;
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                                                                     STRAIN-Y;
                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                          HEAT SHOCK PROTEIN 70
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ilarity 23.2%;
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(TremBLrel. 02, Last sequence update)
(TremBLrel. 17, Last annotation updat
L 29.8 KDA PROTEIN.
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Mitsui Y., Yamman
nadect: Trypanosoma
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SEQUENCE 2
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"Nucleotide sequence of a Trypanosoma cruzi HSP-70 c-DNA.";
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; D87511; BAA13410.1;
HSSP; P08109; ICKR.
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                                                                                                                                                                   Levy Yeyati P., Lafon S., Bonnefoy S., Levi M.;
"Nucleotide sequence of a Trypanosoma cruzi HSP-70
Submitted (APR-1991) to the EMBL/GenBank/DDBJ datab
EMBL; X58715; CAA41551.1; -.
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: September 18, 2002, 16:30:50; Search time 24.1 Seconds (without alignments) 260.272 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-676-718A-1 831 1 MAAGPSGCLVPAFGKRLLLA.....ILKWNTDSVEEFLSEKLERI 162

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

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SE_CYS
                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                      Roethlein D., Kyriakopoulos A., Behne D.; "A 15 kDa-selenoprotein in several tissues of the rat."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
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Q9ERR7;
01-MAR-2002 (Rel. 41,
01-MAR-2002 (Rel. 41,
01-MAR-2002 (Rel. 41,
15 kDa selenoprotein p
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SE_CYS
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20519655; PubMed=10945981;
Kumaraswamy E., Malykh A., Korotkov K.V., Kozyavkin
Kwon S.Y., Moustafa M.E., Carlson B.A., Berry M.J.,
Hatfield D.L., Diamond A.M., Gladyshev V.N.;
"Structure-expression relationships of the 15 kDa se
                                                                                                                                                                                                                                        Selenium;
                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                             SIGNAL
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Selenium; Selenocysteine;
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                                                                                                                                                                                                                                                                                                                                                                           ssible role of the protein in cancer etiology."; Biol. Chem. 275:35540-35547(2000).
                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute.
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          VRGSDPVLKLLDDNGNIAEELSILKWNTDSVEEFILSEKLERI
                                         MAAGOGGWLRPALGLRLILATAFQAASALGAEFASEACRELGFSSNLLCSSCDLLGQFNL
                                                                                                   MAAGPSGCLVPAFGKRLLLATVLQAVSAFGAEFSSEACRELGFSSNLLCSSCDLLGQFNL
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VRGSDPVLKLLDDNGNIAEELSILKWNTDSVEEFLSEKLERI
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93
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                                                                                                                                  Score 749; DB 1;
Pred. No. 6.2e-68;
1; Mismatches 13
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15 KDA SELENOPROTEIN.
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Sciurognathi; Muridae;
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В.J.,
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Matches 25
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EMBL; AL591792; CAC47482.1; -.
PIR; A32888; SYRZET.
HSSP; P27000; 1GLN.
InterPro; IPR000924; tRNA-synt_1c.
InterPro; IPR001412; tRNA-synt_1.
                                                                                                                                   BINDING
CONFLICT
CONFLICT
SEQUENCE
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Capela D., Barloy-Hubler F., Gonzy J., Bothe G., Ampe F., Batut

Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S

Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,

Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,

Renard C., Thebault P., Vandenbol M., Weldner S., Galibert F.;

"Analysis of the chromosome sequence of the legume symbiont

Sinorhizobium meliloti strain 1021.";

Proc. Natl. Acad. Sci. U.S. A. 98:9877-9882(2001).

-I- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +

diphosphate + L-glutamyl-tRNA(Glu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYE_RHIME P15189;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laberge S., Gagnon Y., Bordeleau L.M., Lapointe J.; "Cloning and sequencing of the gltX gene, encoding the synthetase of Rhizobium meliloti A2.";
                                                                                                                                                                                                  SITE
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLTX OR R02903 OR SMC03172.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision;
                                                                                                                                                                                                                                              Aminoacyl-tRNA synthetase;
                                                                                                                                                                                                                                                          pfam; pf00749; tRNA-synt_1c; 1.
prINTS; pr00987; TRNASYNTHGLU.
prOSITE; pS00178; AA_TRNA_LIGASE_I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89291743; PubMed-2661539;
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   364
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                              94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                           KLGRFPQVQAFV-RSD---KPKLFRGLQIKYVRGSDPVLKLLDDNGNIAEEL-SILKWNT 148
KLGELPDLAAFLFKSDLGLQPAAFAGVK----ASPEEMLKILN---TVQPDLEKILEWNK 416
                                                         Similarity 33.8
25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171:3926-3932(1989).
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
MISSING (IN REF. 1).
K -> KQ (IN REF. 2).
K -> KQ CIN REF. 2).
                                                         Score 82; DB
Pred. No. 1.1;
15; Mismatches
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                                                                                    Length 485
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PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Heat shock; Mult
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MEDLINE=90306037; PubMed=2163842;
Macfarlane J., Blaxter M.L., Bishop R.P., Miles M.A.,
"Identification and characterisation of a Leishmania obelonging to the 70-kDa heat-shock protein family.";
Eur. J. Biochem. 190:377-384(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1990 (Rel. 15, Last sequence update) 01-MAY-1991 (Rel. 18, Last annotation update) Heat shock 70 kDa protein.
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PIR; S11448; S11448.
PIR; S11572; S11572.
HSSP; P08107; 1HJO.
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01-AUG-1990
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                                                                                                          DKATLNKEIDVTLEWLSSNQEATKEEYEHKQKEL
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                                                                                                                                                                                                                    MTKDCHLLGTFDLSGIPPAPRGVPQIEVTFD---LDANGILNVSAEEKGTGKRNQITITN
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9 MW; 716D85A2C61FE43B CRC64;
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Pred. No. 1.9;
23; Mismatches
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antigen
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HS70_TRYCR P05456; 01-NOV-1988 01-NOV-1988

(Rel. 09, Created) (Rel. 09, Last seq.

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MEDLINE=88157703; PubMed=2831499;
MEDLINE=88157703; PubMed=2831499;
                                                                                                                                                                            01-JUL-1989 (Rel. 11, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
Heat shock 70 kDa protein 4 (HSP70).
Trypanosoma brucei brucei.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
CCBL_TaxID-5702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00301; HEATSHOCK70.
PROSTTE; PS00297; HSP70_1; 1.
PROSTTE; PS00329; HSP70_2; 1.
PROSTTE; PS01036; HSP70_3; 1.
ATP-binding; Heat shock; Multigene family.
SEQUENCE 680 AA; 73809 MW; D102000F5B7A8D82 CRC64;
                                                                        SEQUENCE FROM N.A. MEDLINE-87089827; Glass D.J., Polver
                                                                                                                                                                                                                                                                                                                                                                   HS74_TRYBB
P11145;
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PIR; A28531; A28531.
PIR; S06158; S06158.
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                        Trypanosoma
                                                Glass D.J., Polvere R.I., van der Ploeg L. "Conserved sequences and transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   509
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37; Conser
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                          brucei."
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6:4657-4666(1986)
                                                                                                   PubMed=3796613;
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LONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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THIG_CAUCR
           C STRAIN-ATCC 19089 / CB15;

X MEDLINE=21173698; PubMed=11259647;

A Nierman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.]

A Nierman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.]

A Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., El.

A Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., El.

A Potocka I., Nelson W.C., Newton A., Schinn M.L., Haft D.H.,

A Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry I.

A Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry I.

A Kolonay J.F., Smit J., Craven M.B., Vamathevan J., Ermolaeva M., While M., While M., Walf A., Vamathevan J., Ermolaeva M., While M., While M., Walf A., Vamathevan J., Ermolaeva M., While M., Walf A., Vamathevan J., Ermolaeva M., While M., Walf A., Vamathevan J., Fraser C.M., While M., Walf A., W
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Best Local
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Q9A746;
16-OCT-2001
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PROSITE; PS00229; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M14697; AAA30204.1; PIR; A25398; A25398.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=69394;
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36; Conserv
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Pred. No. 2.2;
16; Mismatches
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Best Local S
Matches 42
PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Heat shock; Multig VARIANT 81 81 L
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EMBL;
HSSP;
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                                                                                                                                                                                                                                                                            or send an
                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
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MEDLINE-94187793; PubMed-8139614;
BOCK J.H., Langer P.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q07437;
01-FEB-1995
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                                                                                                                                         Pfam;
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Mol. Biochem. Parasitol.
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NCBI_TaxID=5659;
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SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY
                                                                                                                                                                                  L14604;
L14605;
P08107;
                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL
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SEQUENCE FROM N.A.

MEDLINE-95194305; PubMed-7887886;

MEDLINE-95194305; PubMed-7887886;

Kambayashi Y., Takahashi K., Bardhan S., Inagami T.;

"Cloning and expression of protein tyrosine phosphatase-like

"Cloning and expression of protein tyrosine phosphatase-like

derived from a rat pheochromocytoma cell line.";
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SEQUENCE
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SEQUENCE FROM N.A.
MEDLINE-96016179; PubMed-7568143;
Larigan J.D., Genoves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Protein-tyrosine phosphatase-like N precursor (R-PTP-N) (105 kDa islet cell antigen) (ICA105) (PTP IA-2) (PTPLP) (Brain-enriched membrane-associated protein tyrosine phosphatase) (BEM-3).
          Itoh S., Okada M., Nakagawa H.;

Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.

-I-FUNCTION: IMPLICATED IN NEUROENDOCRINE SECRETORY PROCESSES.

INVOLVED IN PROCESSES SPECIFIC FOR NEUROSECRETORY GRAWULES,

AS THEIR BIOGENESIS, TRAFFICKING OR REGULATED EXOCYTOSIS OR

HAVE A GENERAL ROLE IN NEUROENDOCRINE FUNCTIONS. SEEMS TO LA

INTRINSIC ENZYME ACTIVITY (BY SIMILARITY).

-I-FUNCTION: MAY FUNCTION AS A NEGATIVE REGULATOR OF PTPASES IN

NEURONAL TISSUES.
                                                                                                                                                                                                                                                                               "Relationship of the 37,000- and 40,000-M(r) islet antigens in insulin-dependent diabetes phosphatase-like molecule IA-2 (ICA512)."; J. Clin. Invest. 96:1506-1511(1995).
                                                                                                                                                                                                                                                                                                                                       STRAIN-SPRAGUE-DAWLEY: TISSUE-Brain; MEDLINE-95386708; PubMed-7657822; Payton M.A., Hawkes C.J., Christie M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-NOV-1997 (Re
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EMBL; U40652; AAA83235.1; -.
EMBL; D46414; BAA07397.1; -.
EMBL; D45414; BAA08254.1; -.
EMBL; D45414; BAA08254.1; -.
HSSP; P18052; 1YFO.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_prot_phphtase.
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PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000242; Tyr_prot_phphtase. Pfam; PF00102; Y_phosphatase; 1.
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INDUCTION: BY MITOGENS SUCH AS BASIC FIBROBLAST GROWTH FACTOR (BFGF) AND PLATELET DERIVED GROWTH FACTOR (PDGF) (BY SIMILARITY).
PTM: APPEARS TO UNDERGO MULTIPLE PROTEOLYTIC CLEAVAGE AT CONSECUTIVE BASIC RESIDUES (BY SIMILARITY).
SIMILARITY: CONTAINS 1 PROTEIN-TYROSINE PHOSPHATASE DOMAIN.
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  l Similarity
40; Conserv
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KSLPOTSSA

P -> P OFSSA

P -> P OFSSA

R -> P (1

A -> 
                        Score 80;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. ...) (POTENTIAL).

N-LINKED (GLCNAC. ...) (POTENTIAL).

MRRPRRPGGPAGCGGSEGGGLTLYCLLLLSGRPGGCSAI

SAHGCLFDRRLCSHLEVCIQDGLFGQCQAGVGQARPLLQVT

SPYLQRLQGULRQLMSQGL -> MACLDSARQEWGRHGPCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLEAVAGE SITE (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN-TYROSINE PHOSPHATASE-LIKE EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
ced. No. 3.8;
Mismatches
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R (IN REF. 2).

V (IN REF. 2).

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  41;
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                                              Length
                                                                                                                  CRC64;
Indels
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5 PSGCLVPAFGKRLLLATVLQ-----AVSAFGAEFSSEACRELGFSSNLLCSSCDLLGQF 58

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 Query Match
Best Local S
Matches 41
                                                                                                                                                                                                                EMBL; X60060;
PIR; S21877;
                                                                                                            PROSITE; PS01
PROSITE; PS00
ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=92361242; PubMed=1822990;
MCDLINE=92361242; PubMed=1822990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eu Asteridae; euasterids I: Solamalon
                                                                                                                                                                                  InterPro; IPR000886; ER_target.
InterPro; IPR001023; HSP70.
                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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16-OCT-2001 (Rel. 40, Last annotation updat 

Luminal binding protein 1 (Bip 1) (78 kDa 9 

homolog 1) (GRP 78-1) (Fragment).
                                                                                                                                                                       Pfam; PF00012; HSP70;
                                                                                                                                                                                                          HSSP; P19120; 1NGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4097
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01-FEB-1995 (Rel. 31, Last seq
16-CCT-2001 (Rel. 40, Last ann
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                                                                                                                                                                                                                                                                                           European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: PROBABLY PLAYS A ROLE IN FACILITATING MULTIMERIC PROTEIN COMPLEXES INSIDE THE ER.
                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Endoplasmic reticulum lumen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tobacco
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                                                                                                                                                                                                                                  X60060; CAA42662.1;
                                                                                                                                                                                                                                                        s requires a license agreement (S an email to license@isb-sib.ch).
           Similarity
                                                                                                                                              PS00297; HSP70_1; PS00329; HSP70_2;
                                                                                                                                                                                                                                                                             non-profit institutions as long and this statement is not removed.
                                                                                                                       PS01036; HSP70_3; PAPS00014; ER_TARGET;
                                                         241
287
290
                                                                                                                                                                                                                                                                                                                                                                                                       Goldman M.H., Dem 3:1251-1251(1991).
 Conservative
                                                                                                                                                                                                                     S21877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -QVTSPVLQRL--QGVLRQLMSQGLSWHDDLTQYVISQEMERI
                                                                                                         Endoplasmic reticulum; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            luminal binding protein
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           9.4%;
                                                              M.
                                                                                                                                                                                                                                                                                                                                                                                                                   Demolder J.,
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                                                                                                                                  PARTIAL
 Score 78; DB:
Pred. NO. 1.5;
24; Mismatches
                                                          N-LINKED (GLCNAC. . .) (POTENTIAL)
PREVENT SECRETION FROM ER (POTENT);
E80F65136E64BF89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Solanaceae; Nicotiana
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s encoded
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                                                                       (POTENTIAL).
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Gaps
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RESULT 12
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Query Match 9.4
Best Local Similarity 23.0
Matches 41; Conservative
                                                                                                                                                                                                                                             PIR; PQ0262; PQ0262.

HSSP; P19120; 1NGC.
InterPro; IPR000886; EL_target.
InterPro; IPR001023; HSP70.

Pfam; PF00012; HSP70, 1.

PROSITE; PS000297; HSP70_1; PARTIAL.
PROSITE; PS000397; HSP70_2; PARTIAL.
PROSITE; PS00136; HSP70_3; PARTIAL.
PROSITE; PS001036; HSP70_3; PARTIAL.
PROSITE; PS00104; ER_TARGET; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BIP2_TOBAC
Q03682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Denecke J., Goldman M.H., Demolder J., Seurinck J., Plant Cell 3:1251-1251(1991).
-i- FUNCTION: PROBABLY PLAYS A ROLE IN FACILITATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92361242; PubMed-1822990;
Denecke J., Goldman M.H., Demolder J.,
"The tobacco luminal binding protein i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-minal binding protein 2 (BiP 2) (78 kDa glu
homolog 2) (GRP 78-2) (Fragment).
                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                   ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Endoplasmic reticulum lumen. SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MULTIMERIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S21878;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRNTVIPT--KKSQVFTTYQDQQTTVSIQVFEGERS---
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289
292 ;
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                                                                                                                          241
292
32260
                       9.4%;
                                                                                                                                                                                                                        reticulum; Multigene family.
                                                                                                                             MW.
24;
                       Score 78; DB 1;
Pred. No. 1.5;
                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL).
PREVENT SECRETION FROM ER (POTENTIAL).
667A4F5107C6E2D5 CRC64;
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63;
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                                                                                   Complete INIT_MET
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ProDom; PD002691; IIVD_EDD; 1.
PROSITE: PS00886; IIVD_EDD_1; 1.
PROSITE: PS00887; IIVD_EDD_2; 1.
PROSITE: PS00887; IIVD_EDD_3; 1.
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Dihydroxy-acid dehydratase (EC 4.2.1.9) (DAD)
110) (VEG110).
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P51785;
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METAL
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EMBL; 299115; CAB14105.1; -.
Subtilist; BG11532; 11vD.
InterPro; IPR000581; IIvD_EDD.
Pfam; PF00920; IIvD_EDD; 1.
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STRAIN-168 / MARBURG;
MEDLINE-96349105; PubMed-8760912;
MEDLINE-96349105; PubMed-8760912;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restime to the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- COFACTOR: BINDS 1 4FE-4S CLUSTER (POTENTIAL).
-1- PATHWAY: FOURTH STEP IN VALINE AND ISOLEUCINE
-1- SIMILARITY: BELONGS TO THE ILVD / EDD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulation map for Bacillus subtilis.";
Electrophoresis 18:1451-1463(1997).
-i- CATALYTIC ACTIVITY: 2,3-dihydroxy-3-methylbutanoate
                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *Sequence analysis of the Bacillus subtilis chromosome region the serA and kdg loci cloned in a yeast artificial chromosome. Microbiology 142:2005-2016(1996).
                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antelmann H.,
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              IRON-SULFUR (4FE-4S) (POTENTIAL)
IRON-SULFUR (4FE-4S) (POTENTIAL)
CAC59717EB9D7EDA CRC64;
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01-FEB-1995 (Rel. 31, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Luminal binding protein 5 precursor (I
protein homolog 5) (GRP 78-5).
                                                                  PRINTS; PR00301; HEATSHOCK70.
PROSITE; PS00014; ER TARGET; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
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Plant Cell 3:1251-1251(1991)
-I- FUNCTION: PROBABLY PLAYS A ROLE IN FACILITATING
MULTIMERIC PROTEIN COMPLEXES INSIDE THE ER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-92361242; PubMed-1822990;
Denecke J., Goldman M.H., Demolder J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nicotiana tabacum (Common tobacco),
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                             HSSP; P19120; 3HSC
                                                                                                                                                                                                                                                                                                  PIR; S21880; S21880.
PIR; JQ1361; JQ1361.
                                                                                                                                                                                                                                                                                                                                                       EMBL; X60058; CAA42660.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q03685;
                          SIGNAL
                                            ATP-binding;
                                                                                                                                                                                                                           InterPro; IPR000886; InterPro; IPR001023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERRATUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant Cell 3:1025-1035(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The tobacco luminal binding protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Endoplasmic reticulum lumen. SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YVRGSDPV-LKLLDD------
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                                                                                                                                                                                                   PF00012; HSP70;
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ilarity 21.5%;
Conservative 3
               Endoplasmic reticulum; Mu
1 24 POTENTIAL
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Pred. No. 4.5;
33; Mismatches
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                                            Multigene family; Signal.
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BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seurinck
s encoded
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HS70_LEIMA
P14834;
01-APR-1990
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SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-89041551; PubMed-3186441;
Lee M.G., Atkinson B.L., Glannini S.H.,
Lee M.G., atkinson of the hsp 70
                                                                                                                                                                              Pfam; PF00012; HSP70; 1.

PROSITE; PS00297; HSP70_1; 1.

PROSITE; PS00329; HSP70_2; 1.

PROSITE; PS01036; HSP70_3; 1.

ATP-binding; Heat shock; Multigene family.

NON_TER 516 516
                                                                                                                                                                                                                                                                                                                                           EMBL; M36675; AAA29251.1; -. PIR; S06443; S06443. HSSP; P08109; 1CKR.
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01-MAR-2002
                                                                                                                                                                SEQUENCE
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48 LCSSCDLLGQFNLLQLDPDCRGCCQEEAQFETKKLYAGAILEVCGXKLGRFPQVQAFVRS 107
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PREVENT SECRETION FROM ER (POTENTIAL).
7980231A991DC590 CRC64;
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SUMMARIES
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                                                                                                                                                                                                                                            CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Hagan, Patrick J.
REGISTRATION NUMBER: 27,643
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEPAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 661 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08399986B Patent No. 5801041 GENERAL INFORMATION:
                                                              Query Match
Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19103-2307

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Godwin, Andrew TITLE OF INVENTION: NO. 58 TITLE OF INVENTION: Of TURNUMBER OF SEQUENCES: 35
                                                                                                                                                                                         MOLECULE TYPE:
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                                                                                                                                                                                                                                       TYPE: amino acid
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                               8 CLVP------AFGKRLLLATVLQAV-----SAFGAEFSS-----EACRELGFS 44
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of Tumor
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                                                                             Score 79.5; DB Pred. No. 0.35;
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                                                              Indels 139;
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                                                                                                                                                                                                                                                                                                                                       TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 661 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Hagan, Patrick J.
REGISTRATION NUMBER: 27,643
TELECOMMUNICATION INFORMATION:
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HYPOTHETICAL:
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149 EVLGCTSPRLDASKYDAIVYLGDGRFHLESIMIHNPEIEAFQYDPYSRKLTREFYDHDLM 208
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                                 89 CLVPIQNTDGIAMLYVFGKRLVVVSTVQFIPSLQTLRTTFNKDDSSIRIDIPQCKPLSPG 148
                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 22-JUN-1995 CLASSIFICATION: 435
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VENTION: No. 5821338el Gene Associated with Suppression
VENTION: of Tumor Development
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                                                                                                                                  Score 79.5; DB 2;
Pred. No. 0.35;
8; Mismatches 64
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                                                                                                                                      Query Match
Best Local
                                                                                                                         Matches
                                                                                                                                                                                                                                                                           TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
FILING DATE: 06-JUL-1993
ATTORIEY, ASENT INFORMATION:
                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wittrup, I APPLICANT: Robinson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
538
                                                        112 LFRGLQIKYVRGSDPVLKLLDDNGNIAEELSILK 145
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                                                                                    53 DLLGQFNLLQLDPDCRGCCQEEAQFETKKLYAGAILEVCG-XKLGRFPQVQAFVRSDKPK 111
                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                         NAME: DiGiglio, Frank S. REGISTRATION NUMBER: 31,346 REFERENCE/DOCKET NUMBER: 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
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                                                                                                                                                                                                                                                                LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RKNRIGSIEIARKCTTFGLIQGTLGRQGNLKVVEELEAQLERKGKKFLRVLLSEIFPEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NY
                                                                                                                                                                                                                                                                  663 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: SCULLY, SCOTT, MURPHY & PRESSER 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                               516-742-4366
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                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0,
--SEEDIERMVKEAEEFAEEDKILK 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                            SANS UR
                                                                                                                                      8.9%;
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METHODS FOR INCREASING SECRETION
EXPRESSED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----DDNGNIAEELSILKWNTDSVEEFLSEKLERI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/441,139
                                                                                                                      ; Score 74; DB 1; ; Pred. No. 1.7; 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             8646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----FRGLQIKYVRGSDPV 127
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                                                                                                                        37;
                                                                                                                                                     Length 663
                                                                                                                      Indels
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RESULT

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US-08-441-139-2

Sequence 2, Applic Patent No. 5773245

Application US/08441139

GENERAL INFORMATION:
APPLICANT: Wittru
APPLICANT: Robins

Wittrup, Dr. Karl D.
Robinson, Anne S.
ENTION: METHODS FOR INCREASING SECRETION

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; MOLECULE TYPE: protein
US-08-441-139-2
                                                                                                                            Sequence 2, Application US/08942686 Patent No. 6183988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                         GENERAL INFORMATION:
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TELEX: 230 901 SANS U
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: D1619110, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin RelacID DATA: CURRENT APPLICATION NUMBER: US, FILING DATE: 15-MAY-19
               APPLICANT: Bloch, Donald B.
APPLICANT: Bloch, Kenneth D.
TITLE OF INVENTION: LEUKOCYTE-SPECIFIC PROTITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
   CORRESPONDENCE
                                                                                                                                                                                                                                       614 DAANDVLEWLDDNFETAIAEDFD 636
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                                                                                                                                                                                                                                                                                                              554 TQEEIDRMVEEAEKFASEDASIKAKVESRNKLENYAHSLKNQVNGDLGEKLEEEDKETLL 613
                                                                                                                                                                                                                                                                                                                                                                                   497 NLLGKFELTGIPPAPRGVPQIEVTF---ALDANGILKVSATDKGTGKSESITITNDKGRL 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                      53 DLLGQENLLQLDPDCRGCCQEEAQFETKKLYAGAILEVCGXKLGRFPQVQAFVRSDKPKL 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/089,997 FILING DATE: 06-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                               FRGLQIKYVR-----GSDPVLKL------LDD-----NGNIAEEL------ 141
                                                                                                                                                                                                                                                                            ----SILKWNTDSVEEFLSEKLE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
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Garden City
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ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.3%; Score 69; DB
23.1%; Pred. No. 7.3;
ative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RECOMBINANTLY EXPRESSED PROTEINS
                                                   LEUKOCYTE-SPECIFIC PROTEIN AND GENE, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0R 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            38;
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RESULT 6
5196523-13
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5196523-13
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                                                                                                                                                                                                                                                                   ;Patent No. 5196523

APPLICANT: LEE, AMY S.

TITLE OF INVENTION: CONTROL OF GENE EXPRESSION BY GLUCOSE,

CALCIUM AND TEMPERATURE

CALCIUM AND TEMPERATURE
                                                                                           SEQ ID NO:13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
   Query Match
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                        APPLICATION NUMBER: US/07/:
FILING DATE: 19-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 282,880
FILING DATE: 05-DEC-1988
                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 28
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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NAME: GOLDSTEIN, JORGE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 02-OCT-1
CLASSIFICATION: 514
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                   740 FKEVFAIQETNGN 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        681 LKEPMWLDKIKKRLNEHGYPQVEGFVQ-DMRLIFQNHRASYKYKDFGQMGFRLEAEFEKN 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            627 SQCCCQESEVLEROMCPEEQLKCEFLLLKV----YCC-SESSFFAKIPYYYYIREACQG 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 SDPVLKLLDDNGN 136
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OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                        APPLICATION NUMBER: 690,951 FILING DATE: 01-JAN-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 XK----LGR-----FPQVQAFVRSDKPKLFRG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 SSEACRELGFSSNLLCSSCDLLGQFNLLQLDPDCRGCCQEEAQFETKKLYAGAILEVC-G 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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les 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               753 amino acids
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SYSTEM: PC-DOS/MS-DOS
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02-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.0%; Score 66.5;
24.1%; Pred. No. 17;
   7.98;
                                                                                                                                                                                                                 US/07/354,988
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 Score 65.5;
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 DВ
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Length 187;
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       RESULT
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                                                                                                                                                                                                         Query Match
Best Local S
                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
FILING DATE: 06-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: DiGiglio, Frank S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wittrup, I
                                                      534 ---
                                                                                    114 RGLQIKYVRGSDPVLKLLDDNGNIAEELSILKWNTDSVEEFLS 156
                                                                                                                         478 LLGTFDLTGIPPAPRGVPQIEVTFE---IDVNGILRVTAEDKGTGNKNKITITNDQNRL- 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 RGLQIKYVRGSDPVLKLLDDNGNIAEELSILKWNTDSVEEFLS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 27; Conser
                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 8646
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                                                                                                                                                        54 LIGQFNLLQLDPDCRGCCQEEAQFETKKLYAGAILEVCGXKLGRFPQVQAFVRSDKPKLF 113
                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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                                                                                                                                                                                           27; Conserv
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                                                                                                                                                                                           Conservative
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                                                      -TPEEIERMVNDAEKFAEEDKKLKERIDTRNELES 567
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6; Mismatches
                                                                                                                                                                                                       Score 65.5;
Pred. No. 19
                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                             19;
                                                                                                                                                                                                                         DB 1;
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; Sequence 16, Applia
; Patent No. 5773245
                                                                                                                                                                                                         RESULT 9
US-09-357-251-31
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                                                                                                                                                                      Sequence 31, Application US/09357251 Patent No. 6271441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5773245
GENERAL INFORMATION:
                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.9%;
Best Local Similarity 26.2%;
CURRENT APPLICATION NUMBER: US/09/357,251 CURRENT FILING DATE: 1999-07-20 EARLIER APPLICATION NUMBER: 60/093,530
                                                  APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Layo O.
APPLICANT: Orozco, Buddy
APPLICANT: Schwaber, James S.
TITLE OF INVENTION: Plant Aminoacyl-trna Synthetase
FILE REFERENCE: BB-1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
PILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/441,139 FILING DATE: 15-MAY-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                        114 RGLQIKYVRGSDPVLKLLDDNGNIAEELSILKWNTDSVEEFLS 156
                                                                                                                                                                                                                                                                                                                                         490 LLGTFDLTGIPPAPRGVPQIEVTFE---IDVNGILRVTAEDKGTGNKNKITITNDQNRL- 545
                                                                                                                                                                                                                                                                                                                                                                         54 LIGQFNLLQLDPDCRGCCQEEAQFETKKLYAGAILEVCGXKLGRFPQVQAFVRSDKPKLF 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                          -TPEEIERMVNDAEKFAEEDKKLKERIDARNELES 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
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Pred. No. 19;
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Gaps

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: EARLIER FILING DATE: July 21, 1998
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: Microsoft Office 97
: SEQ ID NO 31
: LENGTH: 1072
: TYPE: PRT
: ORGANISM: Saccharomyces cerevisiae US-09-357-251-31
                                                                            RESULT 11
US-09-352-990-27
; Sequence 27, Application US/09352990
; Patent No. 6255090
; GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
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Best Local
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APPLICANT: Famodu, Layo O.
APPLICANT: Orozco, Buddy
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Plant Aminoacyl-tRNA Synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: OH, BOUNG-JUN
APPLICANT: KI, MOON KYUNG
APPLICANT: SHIN, BYONGCHUL
APPLICANT: SHIN, BYONGCHUL
APPLICANT: CHUNG, CHANG HO
TITLE OF INVENTION: SMALL AND CYSTEINE RICH ANTIFUNGAL DEFENSIN
TITLE OF INVENTION: THIONIN-LIKE PROTEIN GENES HIGHLY EXPRESSED
TITLE OF INVENTION: INCOMPATIBLE INTERACTION
EILE REFERENCE: 1942/44
CURRENT APPLICATION NUMBER: US/09/442,631
CURRENT FILING DATE: 1999-11-18
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                                                                                                                                                                                                                                                                                                                                                                                                                          Match 7.8%; Score 64.5; DB 4; Local Similarity 29.3%; Pred. No. 1.3;
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RESULT 12
US-08-162-146-3
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US-09-352-990-27
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EARLIER FILING DATE: July 15, 1998
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Microsoft Office 97
SEQ ID NO 27
LENGTH: 461
TYPE: PRT
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Best Local Similarity
Matches 22; Conserv
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CURRENT APPLICATION NUMBER: US/09/352,990
CURRENT FILING DATE: 1999-07-14
                                                                                              TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR92/
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 91/071
FILING DATE: 12-JUN-1991
ATTORNEY/AGENT INFORMATION:

NAME: WEGNER, Harold C.

REGISTRATION NUMBER: 25,258
                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSE: Foley & Lardner
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DEVINOY, Eve
APPLICANT: THEPOT, Dominique
TITLE OF INVENTION: Production of a Protein of Interest in
TITLE OF INVENTION: the Milk of a Transgenic Mammalian
MOLECULE TYPE:
                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                      TELEPHONE: (202) 672-5399
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                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 10-FEB-1994
                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 TDIDDKIIKRANENG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 EFKPIHAGEVGMYVCGITVYDLCHIGHGRTFVAFDVVARYLR-----FLGYKLKYVRNI 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 ETKKLYAGAI-LEVCGXKL------GR----FPQVQAFVRSDKPKLFRGLQIKYVRG- 123
                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                 linear
                                                                                                                                                             (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.8%; Score 64.5;
29.3%; Pred. No. 15
                                                                                                                                                                                                                                                                                 FR 91/07179
                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/162,146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Suite 500
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; MOLECULE TYPE: protein US-09-314-127-3
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US-09-314-127-3
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Best Local Similarity
Query Match 7.6%; Score 63.5; 1
Best Local Similarity 26.7%; Pred. No. 3.3
Matches 39; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                     TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                 SEQUENCE CHARACTERISTICS
LENGTH: 127 amino acid
                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 25,258
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91/07179
FILING DATE: 12-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DEVINOY, Eve
APPLICANT: THEPOT, Dominique
TITLE OF INVENTION: Production of a Protein of Interest
TITLE OF INVENTION: the Milk of a Transgenic Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 ECRGDKKCCFSRCAMRYL---EPILE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 -- RSDKPKLFRGLQIKYVRGSDPVLK 129
                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 DNDCLGSTVCCPSAAGGSCR-----TPIIVPTPKAGRCPWVQAPMLSQLCEELSDCANDI 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 DPDCRG---CCQEEAQFETKKLYAGAILEVCGXKLGRFPQVQAFV------
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 CLVP-AFGKRLLLATVLQAVSAFGAEFSSEA---CRELGFSSNLLCSSCDLLGQFNLLQL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 CLISLALG---LLA--LEAALALAPKFIAPVQVMCPEPSSSEETLCLS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20007-5109
                                                                                                                                                                                                                                                                                                                   WEGNER, Harold C
                                                                                                                                            amino acids
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                                                                                                                                                                                                                                         (202) 672-5399
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                                                                                                                              linear
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26.7%;
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Pred. No. 3.
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                                    DB 4;
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   45;
                                     Length 127;
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   49;
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                                                                                                                                                                      APPLICATION NUMBER: 07/444490
ETILING DATE: 01-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/290224
ETILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REGISTRATION NUMBER: 00,000
                                                                      TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                  SEQUENCE CHARACTERISTICS:
LENGTH: 718 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,792
FILING DATE: 19-May-1995
CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
08/380227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 720 Kb floppy disk
                                                                                                                          TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                     FILING DATE: 13-JAN-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CITY: South San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 28-MAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/3
FILING DATE: 30-JAN-1995
                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 DNDCLGSTVCCPSAAGGSCR-----TPIIVPTPKAGRCPWVQAPMLSQLCEELSDCANDI 100
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TOPOLOGY:
                                                                                                           TELEFAX:
                                                                                                                        TELEPHONE:
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460 Point San Bruno Blvd
                                                                                                           415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bodary,
                                                                                                                                                                                                                                                                                                                                           13-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                           28-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sarah C.
Cornelia M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           John W.
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US-08-445-042-4
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Patent No. 5726290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: WINPATIN (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,042
FILING DATE: 19-May-1995
CLASSIFICATION DATA:
APPLICATION UNMBER: 08/380227
FILING DATE: 30-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                                       TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 3400
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 720 Kb floppy disk
COMPUTER: LBM PC compatible
COMPUTER: LBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: McLean, CAPPLICANT: Napier, Napier, Napier of INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/218
FILING DATE: 28-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/821
FILING DATE: 13-JAN-1992
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ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/290224
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 07/444490
                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 LRLRPDDSKNFS 127
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                               LENGTH: 718 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                 NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 ALPLGSPRCDLKENLLKDNCAPESIEFPVSEARVLEDRPLSDKGSGDSSQVTQVSPQRIA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 EAQFETKK--LYAGAILEVCGXKLGRFPQVQAFVRSDKPKLFRG----LQIKYVRGSDPV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16
                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RLLLATVLQ--AVSAFGAEFSSEACRELGFSSNLLCSSCDLLGQFNLLQLDPDCRGCCQE 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McLean, John W
                                                                                                                                                                                                                                                                                                                                            01-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sarah C.
Cornelia M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METHOD FOR PREPARING WATER SOLUBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08/218878
                                                                                                                                                                                                                                                                                                                                                                                                                          07/821337
                                                                                                                                                                                                P0552P1C3D1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
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                                                                                                                                                                                                                                                      Query Match 7.6%; Score 63.5; Best Local Similarity 26.5%; Pred. No. 38;
                                                                                                                                                                                                                                      Matches
116 LRLRPDDSKNFS 127
                                     128 LKLL-DDNGNIA 138
                                                                        56 ALPLGSPRCDLKENLLKDNCAPESIEFPVSEARVLEDRPLSDKGSGDSSQVTQVSPQRIA 115
                                                                                                             74 EAQFETKK--LYAGAILEVCGXKLGRFPQVQAFVRSDKPKLFRG----LQIKYVRGSDPV 127
                                                                                                                                                                              16 RLLLATVLQ--AVSAFGAEFSSEACRELGFSSNLLCSSCDLLGQFNLLQLDPDCRGCCQE 73
                                                                                                                                                      RPLWATVLALGALAGVGVG-GPNICTTRGVSS---CQQC-----LAVSPMCAWCSDE 55
                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                15; Mismatches
                                                                                                                                                                                                                                                                           DB 1; Length 718;
                                                                                                                                                                                                                                    61;
                                                                                                                                                                                                                                  Indels 21; Gaps
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Search completed: September 18, 2002, 16:32:47 Job time: 3847 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Comp Compugen Ltd

OM protein protein search, using sw model

Run

September 18, 2002, 15:32:20; Search time 43.02 Seconds (without alignments) 361.843 Million cell update:

cell updates/sec

Perfect score: US-09-676-718A-1 831

Sequence: MAAGPSGCLVPAFGKRLLLA.....ILKWNTDSVEEFLSEKLERI 162

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum Maximum DB DB

seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

Database PIR_71:* pir1:*
pir2:*
pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	. 18	17	16	15	14	13	12	11	10	9	80	7	σ	ۍ	4	ω	2	1	NO.	•
72.5	73	73	73	73	74	74	74	74	74	74.5	74.5	74.5	74.5	75.5	76	76	76.5	76.5	76.5	78	78	78	80	80.5	81	81	81	226.5	Score	
8.7	8.8	8.8	8.8	8.8	8.9	8.9	8.9	8.9	8.9	9.0	9.0	9.0	9.0	9.1	9.1	9.1	9.2	9.2	9.2	9.4	9.4	9.4	9.6	9.7	9.7	9.7	9.7	27.3	Match	
228	1120	346	293	273	996	979	663	663	275	667	667	656	516	261	668	265	664	653	558	484	292	290	269	661	680	668	653	158	Tength	
ν	ພ	N	N	2	N	1	N	N	N	N	N	2	N	2	N	N	N	N	N	_	N	ผ	N	N	N	N	N	N	<u> </u>	}
S17349	H71664	A12229	S21881	T47601	148721	JC2349	T38155	S20877	F82761	D44261	S24782	JN0666	S06443	S14875	S21880	S77181	T06598	S52727	D69644	SYRZET	S21878	S21877	C87482	A25398	S06158	T46574	S11448	E86191	<u> </u>	!
dnaK-type molecula	transcription-repa		4	class IV chitinase	PTP 35 protein - m	protein-tyrosine-p	78 kd glucose regu	dnaK-type molecula							dnak-type molecula			dnak-type molecula	dihydroxy-acid deh	glutamatetRNA li			prote				dnak-type molecula	al pro	Description	

4 5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
70.5	70.5	70.5	70.5	70.5	70.5	71	71	71	71	72	72	72	72.5	72.5	72.5
8.5	æ 5	8.5	8.5	8 .5	æ .5	8.5	8.5	8.5	5	8.7	8.7	8.7	8.7	8.7	8.7
658	644	432	432	272	212	691	899	560	421	777	663	467	1192	830	667
N	N	N	N	N	N	N	N	ν	N	N	2	N	N	N	N
S38890	S67431	S71072	S71074	S59389	H84979	T32748	S71171	T40608	F84450	C85065	T04078	JQ0966	T48499	T18860	S21879
dnak-type molecula	dnaK-type molecula	asparaginetRNA l	asparaginetRNA l	probable membrane	hypothetical prote	hypothetical prote	dnaK-type molecula	conserved hypothet	hypothetical prote	kinesin-like prote	dnaK-type molecula	dnaK-type molecula	receptor-like prot	hypothetical prote	dnaK-type molecula

## ALIGNMENTS

hypothetical protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C;Accession: E86191
C;Accession: E86191
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A;Authors: Hunter, J.L.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia A;Authors: Salzberg, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: E86191
A;Accession: E86191
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A;Accession: E86191

A;Status: preliminary

A; Molecule type: DNA A; Residues: 1-158 <STO>

A;Cross-references: ;Genetics: GB:AE005172; NID:g4836919; PIDN:AAD30621.1; GSPDB:GN00141

A; Map position:

Query Match
Best Local Similarity
Matches 48; Conserv Conservative 27.3%; Score 226.5; 32.9%; Pred. No. 6.1e tive 37; Mismatches .le-15; DB 2; 54; Length Indels 158; 7; Gaps 4.

Ş 17 LLLATVLQAVSAFGAEFSSEACRELGFSSNLLCSSCDLLGQF-NLLQLDPDCRGCCQEEA 75

밁 13 LILASTISAKE----QLSTKECEDLGFSGLALCSDCHSLSEYVKDQELVSDCLKCCADDS 68

밁 Q 69 76 QFETKKL-YAGAILEVCGXKLGREPQVQAFVRSDKPKLFRGLQIKYVRGSDPVLKLLDDN 134 EDSMSKYTYSGAILEVCMRKLVFYPEIVGFIEEEKEK-FPSVKVQYIFNSPPKLIMLDED 127

δÃ 135 GNIAEELSILKWNTDSVEEFLSEKLE 160

맔 128 GEHKESIRIDNWKREHLLQYMREKVK 153

RESULT S11448

dnaK-type molecular chaperone hsc70 - Leishmania donovani
N;Alternate names: heat shock cognate protein 70
C;Species: Leishmania donovani
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 20-Aug-1999
C;Accession: S11448; S11572 R; MacFarlane, Blaxter, M.L.; Bishop, R.P.; Miles, M.A.; Kelly, J.M. 190, 377-384, 1990

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R; MacFarlane, J. submitted to the EMBL Data A; Reference number: S11572
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A;Title: Water-stress regulation and molecular analysis of the soybean BIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dnaK-type molecular chaperone BiP precursor [similarity] - soybean
N;Alternate names: endoplasmic reticulum HSC70-cognate binding protein
C;Species: Glycine max (soybean)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Description: involved in protein folding C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-653 <MAC1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Identifica
A; Reference number:
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A; Accession: T46574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X52314; NID:g9495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-208, 'S', 210-653 <MAC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: X52314
                                                                                                                                                                                                                                                                                            A; Gene:
                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:AF031241; PIDN:AAB86942.1
A;Experimental source: strain Roonoke; clone cUFVB
                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-668 <FIG>
                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Ma
Best Loc
Matches
                                                                                                                                                                                                             ;Keywords: ATP; endoplasmic reticulum; molecular chaperone; stress-induced;1-27/Domain: signal sequence #status predicted <SIG>;28-668/Product: dnaK-type molecular chaperone BIP #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Function
                                                                                                                                                                                                                                                                     Superfamily: heat shock protein 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: S11448
                                                                                                                           Matches
                                                                                                                                                                                                                                                  Keywords: ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 11-May-2000
                                                      446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451
                    59
                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 LCSSCDLLGQFNLLQLDPDCRGCCQEEAQFETKKLYAGAILEVCGXKLGRFPQVQAFVRS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKATLNKEIDVTLEWLSSNQEATKEEYEHKQKEL 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MTKDCHLLGTFDLSGIPPAPRGVPQIEVTFD---LDANGILNVSAEEKGTGKRNQITITN 507
PRNTVIPT -- KKSQVFTTYQDQQTTVSIQVFEGERS
                                                                                     PSGCLVPAFGKRLLLATVLQ-----AVSAFGAEFSSEACRELGFSSNLLCSSCDLLGQF 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --GNIAEELSI-LKW---NTDSVEEFLSEKLERI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKPKLFR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKGRLSKDETERMVNDAMKYEADDRAQRDRVEAKNGLENYAYSMKNTLGDSNVSGKLDDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                           26;
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Pred. No. 6.
                                                                                                                                            Score 81; DB Pred. No. 6.5;
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                                                                                                                                                                                                                                                                                                                                                                                                 GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                           clone cUFVBIP1;
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5.3;
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                                                                                                                                                           Length 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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509

DKPKLFRGLQIKYVR----

DKGRLSRAEIERMVREAAKYEAEDKDQVRQIDAKNGLENYAFSMKNAVNDPNVAGKIEEA

MTKDCHLLGTFELSGIPPPPRGVPQIEVTFD---LDANGILNVSAEEKGTGKRNQIVLTN 508

-GSDPVLKLLDDNG----

NIAEEL -- S

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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-46, 'T',48-63, 'T',65,'SP',68-167,'M',169-178,'R',180-240,'S',242-256,'T'
518-522,'S',524-529,'S0',532-533,'E',535,'RER',539-554,'T',556-557,'E',559-570,'N',57
A;Cross-references: EMBL:X67716; NID:g10625; PIDN:CAA47952.1; PID:g10626
A;Experimental source: strain Brazil
R;Engman, D.M.; Sias, S.R.; Gabe, J.D.; Donelson, J.E.; Dragon, E.A.
Mol. Blochem. Parasitol. 37, 285-287, 1989
A;Title: Comparison of HSP70 genes from two strains of Trypanosoma cruzi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: the sequence is revised in GenBank entry TCHSP70, release 111.0, (PIDN: R:Yang, S.; Bergman, L.W.; Scholl, D.R.; Rowland, E.C. submitted to the EMBL Data Library, August 1992
A;Description: Cloning and characterization of cDNA encoding glucose-regulated A;Reference number: $25648
A;Accession: $25649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Experimental source: strain Maracai
R;Requena, J.M.; Lopez, M.C.; Jimenez-Ruiz, A.; de la Torre, J.C.; Alonso, C.
Nucleic Acids Res. 16, 1393-1406, 198
A;Title: A head-to-tail tandem organization of hsp70 genes in Trypanosoma cruzi.
A;Reference number: A28531; MUID:88157703
A;Accession: A28531
                                                                                                                                                                                 C; Superfami
C; Keywords:
                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-46,'T',48-63,'T',65-167,'M',169-240,'S',242-256,'T',258,'SQ',261-310,
'SQ',532-533,'E',535,'RER',539-551,'V',553-554,'T',556-557,'E',559-570,'N',572-581,
A;Cross-references: GB:M26595; NID:g162116; PIDN:AAA30205.1; PID:g162117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: A44979; MUID:90114336
A;Accession: A44979
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A; Residues: 222-473,'L',475-521,550-622,'A',624-630,'S',632-680 <REQ>
A; Cross-references: GB:X07083; GB:X13690; NID:g10621; PIDN:CAA30115.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type:
A; Residues: 1-68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N; Alternate names: heat shock
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                                                                                                                                                                                                            A;Description: involved in protein folding C;Superfamily: heat shock protein 70
                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
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                                                                                                                                                                                                                                                                                         ;Gene: hsp70
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                                                                                                                                                                                                                                                                   ;Function:
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LCSSCDLLGQFNLLQLDPDCRGCCQEEAQFETKKLYAGAILEVCGXKLGRFPQVQAFVRS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KYVRGSDPVLKLLDDNGNIAEELSILKWNTD--
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                                                                                                                                                                                    ATP;
                                                   37; Conser
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S06158
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                                                                       Score 81;
Pred. No.
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                                                   Mismatches
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                                                                                                     Length 680
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Mol. Cell. Biol. 6, 4657-4666, 1986
A;Title: Conserved sequences and transcription of the hsp70
A;Reference number: A25398; MUID:87089827
A;Accession: A25398: MUID:87089827
A;Molecule type: DNA
A;Residues: 1-661 <GLA>
A;Cross-references: GB:M14697
C;Function:
A:Description: involved in protein folding and assembling/di:C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                   R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koln, J.; Ermolaeva, White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S. A. 98, 4136-4141, 2001

A; Title: Complete Genome Sequence of Caulobacter crescentus.

A; Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                            A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-269 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thiG protein [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
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C; Superfamily:
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C;Species: Trypanosoma brucel
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 13-Mar-1998
C;Accession: A25398
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                                                                                 Query Match
Best Local S
Matches 42
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Best Local S
Matches 36
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                                       LVPAFGKRLLLATVLQAVSAFGAEFSSEACRELGFSSNLLCSSCDLL------GQFNLLQ 62
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LIVGTGKYKDYATNAAAARAAGAEIVTVAVRRV----NLTDPSQPLLVDYVKPTEFTYL- 83
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                                                                                                    9.6%;
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rotein 70
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Pred. No. 7.2;
16; Mismatches
                                                                                                    Score 80;
Pred. No.
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                                                                               Mismatches
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                                                                                                                    DB 2;
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dnaK-type molecular chaperone blp2 - common tobacco (fragment) N; Alternate names: luminal binding protein blp2 C; Species: Nicotiana tabacum (common tobacco) C; Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_chang c; Accession: PQ0262; S21878 R; Demecke, J.; Goldman, M.H.S.; Demolder, J.; Seurinck, J.; Bo Plant Cell 3, 1025-1035, 1991 A;Title: The tobacco luminal binding protein is encoded by a m A; Reference number: JQ1360; MUID:92361242 A; Accession: PQ0262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: heat shock protein 70
C;Keywords: ATP; endoplasmic reticulum; molecular
F;287-290/Region: endoplasmic reticulum retention
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A;Title: The tobacco luminal binding protein A;Reference number: JQ1360; MUID:92361242
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A; Residues: 263-290 <
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: luminal binding protein blp1 c;Species: Nicotiana tabacum (common tobacco) C;Date: 07-Apr-194 #sequence_revision 07-Apr-19C;Accession: S21877; pQ0264
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation of the nucleotide
                                                                                                                                                                                                                                                                                                                                                                     DLTGIAPAPRGTPQIEVTFEVD--
                                                                                                                                                                                                                                                                                                                                                                                                         NLLQLDPDCRGCCQEEAQFETKKLYAGAILEVCGXKLGRFPQVQAFVRSDKPKLFRGLQI 118
                                                                                                                                                                                                                                                                                       ----SQEEIERMVREAEEFAEEDKKVKERIDARNSLETYVYNMKNQINDKDKLADKLE
                                                                                                                                                                                                                                                                                                                            KYVRGSDPVLKLLDDNGNIAEELSILKWNTD---SVEEF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRNTVIPT - - KKSQVFTTYQDQQTTVSIQVFEGERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSGCLVPAFGKRLLLATVLQ-----AVSAFGAEFSSEACRELGFSSNLLCSSCDLLGQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- PNTAGCFTGEDAVRTLRLAREAGGWDLVKLEVLSDPKTLFPDMEETLRSLKLLVADGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 78;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                     -ANGILNVKAEDKGTGKSEKITITNDKGRL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chaperone
                                                                                                                               #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 290
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                                                  a multigene family
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                                                                                           Botterman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Botterman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PID:g19805
otterman, J.
                                                                                                                               20-Aug-1999
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A;Residues: 1-292 CDE2>
A;Cross-references: EMBL:X60059; NID:g19806; PIDN:CAA42661.1; PID:g19807
A;Note: translation of the nucleotide sequence is not complete
C;Genetics:
A;Gene: blp2
C;Function:
A;Description: involved in protein folding and assembling/disassembling curation steps in vivo
C;Superfamily: heat shock protein 70
C;Keywords: ATP: endoplasmic reticulum; molecular chaperone
F;289-292/Region: endoplasmic.reticulum retention signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Laberge, S.; Gagnon, Y.; Bordeleau, L.M.; Lapointe, J.
J. Bacteriol. 171, 3926-3932, 1989
A; Title: Cloning and sequencing of the gltx gene, encoding the glutamyl-tal reference number: A32888; MUID:89291743
A; Accession: A32888
A; Accession: A32888
A; Accession: A32888
A; Molecule type: DNA
A; Residues: 1-484 < LAB>
A; Cross-references: GB:M27221; NID:g341649; PIDN:AAC35209.1; PID:g717082
A; Experimental source: strain A2
C; Superfamily: glutamate--tRNA ligase; glutamine--tRNA ligase homology
C; Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis
F; 6-320/Domain: glutamine--tRNA ligase homology < EGL>
F; 256/Binding site: ATP (Lys) #status predicted
  dihydroxy-acid dehydratase ilvD - Bacillus subtilis C;Species: Bacillus subtilis C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_C;Accession: D69644
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.;
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glutamate--tRNA ligase (EC 6.1.1.17) - Rhizobium meliloti
N;Alternate names: glutamyl-tRNA synthetase
C;Species: Rhizobium meliloti
C;Date: 30--Jun-1992 #sequence_revision 30-Jun-1992 #text_change
C;Accession: A32888
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                  94 KLGRFPQVQAFV-RSD---KPKLFRGLQIKYVRGSDPVLKLLDDNGNIAEEL-SILKWNT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
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                                                                                                                                                                                                                                                                 DSVE-----EFLSEKLERI 162
                                                                                                                                                                                                                                                                                                            KLGELPDLAAFLFKSDLGLQPAAFAGVK----ASPEEMLKILN---TVQPDLEKILEWNK 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLTGIAPAPRGTPQIEVTFEVD---ANGILNVKAEDKGTGKSEKITITNDKGRL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KYVRGSDPVLKLLDDNGNIAEELSILKWNTD---SVEEF------LSEKLE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NLLQLDPDCRGCCQEEAQFETKKLYAGAILEVCGXKLGRFPQVQAFVRSDKPKLFRGLQI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRNTVIPT -- KKSQVFTTYQDQQTTVSIQVFEGERS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSGCLVPAFGKRLLLATVLQ-----AVSAFGAEFSSEACRELGFSSNLLCSSCDLLGQF 58
                                                                                                                                                                                                                         DSIETELRASERMGKKLKAV 436
                                                                                                                                                                                                                                                                                                                                                                                               L Similarity
25; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQEEIERMVREAEEFAEEDKKVKERIDARNSLETYVYNMKNQINDKDKLADKLE 220
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          Score 78; DB
Pred. No. 8.9;
18; Mismatches
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Pred. No.
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                                                                 05-Dec-1997 #text_change 20-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 484
      B.,
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; Alloni, G.; Aze
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glutamyl-tRNA
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                        Azevedo,
      Carter,
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  V.; Berter
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451 MTKDCHLLGTFDLSGIPPAPRGLPQIEVTFD-

LCSSCDLLGQFNLLQLDPDCRGCCQEEAQFETKKLYAGAILEVCGXKLGRFPQVQAFVRS 107

--LDANGILNVSAEEKGTGKRNQITITN 507

Matches

Similarity

Conservative

14;

Mismatches

35;

Indels

13;

Gaps

2

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Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dnaK-type molecular chaperone hsp70 - Leishmania donovani infantum (fragment)
N;Alternate names: heat shock protein hsp70; immunodominant antigen
C;Species: Leishmania donovani infantum
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C;Superfamily: dihydroxy-acid dehydratase
                                                                                                                                               A;Description: involved in protein folding C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-653 <QUI>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A; Accession: S52727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Quijada, L.; Requena, J.M.; Soto, M.; Alonso, submitted to the EMBL Data Library, March 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Aug-1999
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A; Residues: 1-558 < KUN>
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                                                                                                                                                                                                                                                           C; Function:
                                                                                                                                                                                                                                                                                            A;Gene: hsp70
                                                                                                                                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Description: In canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: S52727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references:
   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 YVRGSDPV-LKLLDD------NGNIAEELSILKWNTDSVEEFLSEKLERI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 VSGGPMAAGRTSYGRKISLSSVFEGVGAYQAGKINENELQELEQFGCPTCGSCS--GMFT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 DIKPRDIVTVKAIDNAFALDMALGGSTNTVLHTLALANEAGVEYSLERINEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary
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249-256, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                           EMBL: X85798; NID: g758135; PIDN: CAA59793.1;
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9.2%;
27.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33; Mismatches
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Pred. No. 15;
Score 76.5;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -LGLALPGNGTILATSPERKEFVRKSAAQLMETIR-K
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                                                                                                                                                                                                                  of protein
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C;Species: Glycine max (soybean)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_ch
C;Accession: T06598
R;Kalinski, A.; Rowley, D.L.; Loer, D.S.; Foley, C.; Buta,
Planta 195, 611-621, 1995
                                                                                                                                                                                                                                                            C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Description: involved in protein folding and assembling/disassembling of C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone
                                                             A; Molecule type: DNA
A; Residues: 1-265 <KAN>
A; Cross-references: EMBI
A; Note: the nucleotide:
                                                                                                                       A; Accession: S77181
A; Status: nucleic acid sequence
                                                                                                                                                                                                     DNA Res.
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A;Experimental source:
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dnaK-type molecular chaperone BiP-A - s
N;Alternate names: binding protein BiP
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                                                                                                                                           A;Reference number: S74322; MUID:97061201
A;Accession: S77181
                                                                                                                                                                                          A;Title:
                                                                                                                                                                                                                                    R; Kaneko,
                                                                                                                                                                                                                                                                                                             hypothetical protein slr1809 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-664 < KAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: Z15624; A; Accession: T06598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Binding-protein expression is subject to
                                                                                                                                                                                                     ;Accession: S77181
;Kaneko, T.; Sato, S.; Kotani,
;K.; Okumura, S.; Shimpo, S.;
NA Res. 3, 109-136, 1996
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59
                                                                                                                                                                                3, 109-13
                                                                             references: EMBL:D90908;
                                                                                                                                                                                                                                                                                                                                                                                            EALEWLDDNQSVEKRYEEKLKEV
                                                                                                                                                                                                                                                                                                                                                                                                                       SILKWNTD--SVEEFLSEKLERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RMVREAEEFAEEDKKVKERIDARNSLETYVYNMKNQVSDKDKLADKLESDEKEKVETAVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSGCLVPAFGKRLLLATVLQ-----AVSAFGAEFSSEACRELGFSSNLLCSSCDLLGQF 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKGRL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KYVRGSD-----PVLKLLD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NLLQLDPDCRGCCQEEAQFETKKLYAGAILEVCGXKLGRFPQVQAFVRSDKPKLFRGLQI 118
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45; Conserv
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se: strain Century 84; leaf
                                                               sequence
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23
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 .18;
                                                                                                                                                                                                                                                                                                             Synechocystis sp.
                                                                                                                           not
                                                                                                                                                                                                                  H.; Tanaka, A.; Asa
Takeuchi, C.; Wada,
                                                             ; GB:AB001339;
was submitted
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 Score
Pred.
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Pred.
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No. 18
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 76;
No.
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7.1;
                                                                                                                                                                                     the unicellular cyanobacterium
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                                                          NID:g1652725; PIDN:BAA17739.1; to the EMBL Data Library, June
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                                                                                                                                                                                                                  Asamizu,
Vada, T.; V
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              Length
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                                                                                                                                                                                                                  Miyajima, N.;
da, M.; Yasuda
                                                                                                                                                                                   Synechocysti
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                                                             PID:d10184;
1996
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                                                                                                                                                                                                                                                                                                                                                                                                                   uration steps in vivo C; Superfamily: heat shock protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-653, 'G', 655-668 <DEW>
A; Note: translation of the nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Denecke, J.; Goldman, M.H.S
Plant Cell 3, 1025-1035, 1991
A;Title: The tobacco luminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Denecke, J.; Goldman, M.H.; Demolder, J.; S
submitted to the EMBL Data Library, June 1991
A;Description: The luminal binding protein (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Nicotiana tabacum (common tobacco)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dnaK-type molecular chaperone blp5 precursor - (
N;Alternate names: luminal binding protein blp5
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A; Residues: 1-668 < DEN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession:
                                                                                                                                                                                                                                                                                                                Query Match
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                   15
                                                                                                                                                                                                                                              G
                                                                                                                                       DLTGIAPAPRGTPQIEVTFEVD---ANGILNVKAEDKASGKSEKITITNDKGRL-----
                                                                  ----SQEEIERMVKEAEEFAEEDKKVKERIDARNSLETYVYNMRNQINDKDKLADKLE
                                                                                                                                                                         NLLQLDPDCRGCCQEEAQFETKKLYAGAILEVCGXKLGRFPQVQAFVRSDKPKLFRGLQI 118
                                                                                                                                                                                                           PRNTVIPT -- KKSQVFTTYQDQQTTVTISVFEGERS------LTKDCRLLGKF 491
                                                                                                                                                                                                                                          PSGCLVPAFGKRLLLATVLQ-----AVSAFGAEFSSEACRELGFSSNLLCSSCDLLGQF 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STIEAQNDTIAQLMGEQEALRREFDTLISQQLQENRLNGDRLENLQARLKALEEKIK 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IKYVRGSDPVLKLLDDNGNIAEELSIL----
                                                                                                    KYVRGSDPVLKLLDDNGNIAEELSILKWNTD---SVEEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAEFRRRQKRYFRTIVGSLMFAGAIL--CGGGIYLLSQGGLP----FVIEEKARL-ENLQ 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAQFETKK------LYAGAILEVCGXKL-----GRFPQVQAFVRSDKPKLFRGLQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AELDDAIAFNPGESKFLLSSAEAYLGKWKQHHRAPDADQMHLRVRQCLSLEPGCEGALDL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEFSSEACRELGFSSNLLCSSCDLLGQF--
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                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      involved in
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                              9.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein folding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l binding protein MUID:92361242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pemolder, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                            Score
Pred.
                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-Apr-1994 #text_change
                                                                                                                                                                                                                                                                                            76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BiP) is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seurinck, J.; Botterman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIDN:CAA42660.1; PID:g19813; Seurinck, J.; Botterman, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -KWNTDSVEEF-----LSEKLE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is
                                                                                                                                                                                                                                                                                                                                                                                                                                                    assembling/disassembling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoded
                                                                                                                                                                                                                                                                            64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not
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                                                                                                                                                                                                                                                                                                              Length 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoded by a multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tobacco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             multigene family.
                                                                                                      -LSEKLE
                                                                                                                                                                                                                                                                            50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in
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dnaK-type molecular chaperone hsp70 - w;Alternate names: heat shock protein C;Species: Trypanosoma cruzi C;Date: 07-Apr-1994 #sequence_revisior C;Accession: S14875

#sequence_revision

07-Apr-1994 #text_change 20-Aug-1999

Trypanosoma 70

cruzi

(fragment)

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R:Levy Yeyati, P.; Lafon, S.; Bonnefoy, S.; Levi, M.
submitted to the EMBL Data Library, April 1991
A:Description: Nucleotide sequence of a Trypanosoma cruzi HSP-70 c-DNA.
A:Reference number: S14875
A:Recession: S14875
A:Reces
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